

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:30:15 ; Search time 35.1493 Seconds
(without alignments)
120.578 Million cell updates/sec

Title: US-09-641-802-8
Perfect score: 82
Sequence: 1 LKPFPPKLKVEVFPPF 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 422553

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query						
No.	Score	Match	Length	DB	ID				Description
1	82	100.0	15	4	AAB72507				Aab72507 Colostrin
2	82	100.0	15	4	AAB59313				Aab59313 Ewe colos
3	82	100.0	15	4	AAB72253				Aab72253 Colostrin
4	82	100.0	15	4	AAB72539				Aab72539 Colostrin
5	82	100.0	15	5	AAO14584				Aao14584 Neural ce
6	82	100.0	15	5	AAM51043				Aam51043 Colostrin
7	82	100.0	15	5	AAE20235				Aae20235 Colostrin
8	82	100.0	16	4	AAB59344				Aab59344 Ewe colos
9	37.5	45.7	14	2	AAW48879				Aaw48879 Cyclic pe

10	37.5	45.7	14	2	AAW48904	Aaw48904	Cyclic pe
11	37	45.1	18	4	ABB41738	Abb41738	Peptide #
12	37	45.1	18	4	AAM35535	Aam35535	Peptide #
13	37	45.1	18	4	ABB25488	Abb25488	Protein #
14	37	45.1	18	4	AAM75423	Aam75423	Human bon
15	37	45.1	18	4	AAM62611	Aam62611	Human bra
16	37	45.1	18	4	ABG57176	Abg57176	Human liv
17	37	45.1	18	5	ABG45003	Abg45003	Human pep
18	36	43.9	18	4	AAB72520	Aab72520	Colostrin
19	36	43.9	18	4	AAB59330	Aab59330	Ewe colos
20	36	43.9	18	4	AAB72267	Aab72267	Colostrin
21	36	43.9	18	4	AAB72552	Aab72552	Colostrin
22	36	43.9	18	5	AAO14598	Aao14598	Neural ce
23	36	43.9	18	5	AAM51056	Aam51056	Colostrin
24	36	43.9	18	5	AAE20249	Aae20249	Colostrin
25	34.5	42.1	10	4	AAE07188	Aae07188	Colostrin
26	34.5	42.1	11	4	AAE07198	Aae07198	Modified
27	34.5	42.1	14	2	AAW48877	Aaw48877	Cyclic pe
28	34.5	42.1	14	2	AAW48878	Aaw48878	Cyclic pe
29	34	41.5	10	4	AAE07187	Aae07187	Colostrin
30	34	41.5	15	4	AAB72504	Aab72504	Colostrin
31	34	41.5	15	4	AAB59322	Aab59322	Ewe colos
32	34	41.5	15	4	AAB72250	Aab72250	Colostrin
33	34	41.5	15	4	AAB72536	Aab72536	Colostrin
34	34	41.5	15	5	AAO14581	Aao14581	Neural ce
35	34	41.5	15	5	AAM51040	Aam51040	Colostrin
36	34	41.5	15	5	AAE20232	Aae20232	Colostrin
37	34	41.5	16	4	AAB59352	Aab59352	Ewe colos
38	33.5	40.9	14	2	AAW48905	Aaw48905	Cyclic pe
39	33	40.2	14	2	AAR58339	Aar58339	Hypotensi
40	32.5	39.6	14	2	AAW48906	Aaw48906	Cyclic pe
41	32	39.0	9	5	ABJ01855	Abj01855	158P1D7 r
42	32	39.0	9	5	ABJ01751	Abj01751	158P1D7 r
43	32	39.0	9	5	ABJ01996	Abj01996	158P1D7 r
44	32	39.0	10	5	ABJ01907	Abj01907	158P1D7 r
45	32	39.0	10	5	ABJ01366	Abj01366	158P1D7 r
46	32	39.0	16	2	AAW38528	Aaw38528	S. pneumo
47	32	39.0	16	5	ABB77148	Abb77148	Classical
48	32	39.0	16	6	ABP82437	Abp82437	G protein
49	32	39.0	17	6	AAE34141	Aae34141	T-cell st
50	31.5	38.4	12	2	AAR93361	Aar93361	LYN prote
51	31.5	38.4	14	2	AAW48876	Aaw48876	Cyclic pe
52	31.5	38.4	14	5	ABB81248	Abb81248	GS14K4 an
53	31.5	38.4	17	4	AAU01835	Aau01835	Wheat Gli
54	31	37.8	13	4	AAB74265	Aab74265	Exemplary
55	31	37.8	13	4	AAB80871	Aab80871	Angiostat
56	31	37.8	13	5	ABG97548	Abg97548	Antiangio
57	30.5	37.2	15	2	AAR93461	Aar93461	GST-PI3K
58	30.5	37.2	17	4	AAU01804	Aau01804	Wheat A-g
59	30.5	37.2	17	4	AAU01816	Aau01816	Wheat Gli
60	30.5	37.2	17	4	AAU01798	Aau01798	Wheat A-g
61	30.5	37.2	17	4	AAU01803	Aau01803	Wheat A-g
62	30.5	37.2	17	4	AAU01802	Aau01802	Wheat A-g
63	30.5	37.2	17	4	AAU01806	Aau01806	Wheat A-g
64	30.5	37.2	17	4	AAU01817	Aau01817	Wheat Gli
65	30.5	37.2	18	6	ADA52276	Ada52276	Lymphocyt
66	30	36.6	15	8	ADE75392	Ade75392	Bovine al

67	30	36.6	17	6	ABR81806	Abr81806	MPIV1 WT
68	29	35.4	10	3	AAB03889	Aab03889	Human ART
69	29	35.4	12	2	AAy43069	Aay43069	Thyroid h
70	29	35.4	12	2	AAy43071	Aay43071	Recombina
71	29	35.4	12	3	AAy58310	Aay58310	Rat wild-
72	29	35.4	12	3	AAy58312	Aay58312	Human wil
73	29	35.4	12	3	AAy58308	Aay58308	Human wil
74	29	35.4	12	5	AAO20860	Aao20860	Coactivat
75	29	35.4	12	5	AAO20861	Aao20861	Coactivat
76	29	35.4	14	2	AAR93455	Aar93455	GST-PI3K
77	29	35.4	15	4	AAG62670	Aag62670	Human GVP
78	29	35.4	18	4	AAU01128	Aau01128	Human p69
79	28.5	34.8	14	2	AAW48901	Aaw48901	Cyclic pe
80	28	34.1	8	5	AAU87021	Aau87021	Neck regi
81	28	34.1	8	5	AAU87020	Aau87020	Neck regi
82	28	34.1	9	5	ABJ01633	Abj01633	158P1D7 r
83	28	34.1	10	4	AAE07197	Aae07197	Modified
84	28	34.1	10	5	ABG69554	Abg69554	Human CRP
85	28	34.1	10	5	ABJ01656	Abj01656	158P1D7 r
86	28	34.1	10	5	ABJ01569	Abj01569	158P1D7 r
87	28	34.1	11	2	AAW48881	Aaw48881	Cyclic pe
88	28	34.1	12	2	AAR10937	Aar10937	Residues
89	28	34.1	14	4	AAB72297	Aab72297	ADAMTS-R1
90	28	34.1	15	4	AAG78795	Aag78795	Human myo
91	28	34.1	15	6	ABR38016	Abr38016	Human can
92	28	34.1	15	6	ABR37901	Abr37901	Human can
93	28	34.1	15	6	ABR37915	Abr37915	Human can
94	28	34.1	15	6	ABR37949	Abr37949	Human can
95	28	34.1	15	6	ABR37801	Abr37801	Human can
96	28	34.1	15	6	ABR37944	Abr37944	Human can
97	28	34.1	16	5	AAE21189	Aae21189	Human sol
98	28	34.1	18	6	AAE34144	Aae34144	T-cell st
99	27.5	33.5	14	2	AAW48903	Aaw48903	Cyclic pe
100	27	32.9	8	2	AAR53626	Aar53626	Opioid pe

ALIGNMENTS

RESULT 1

AAB72507

ID AAB72507 standard; peptide; 15 AA.

XX

AC AAB72507;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #8.

XX

KW Dermatological; oxidative stress regulator; colostrinin.

XX

OS Unidentified.

XX

PN WO200112650-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022665.
 XX
 PR 17-AUG-1999; 99US-0149310P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2001-218342/22.
 XX
 PT Modulating oxidative stress level in a cell, involves contacting the cell
 PT with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations.
 XX
 PS Claim 6; Page 25; 48pp; English.
 XX
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVFPPF 15
 |||||
 Db 1 LKPFPKLKVEVFPPF 15

RESULT 2
 AAB59313
 ID AAB59313 standard; peptide; 15 AA.
 XX
 AC AAB59313;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Ewe colostrinin peptide fragment A-4.
 XX
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 OS Ovis sp.
 XX
 PN WO200075173-A2.
 XX
 PD 14-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-GB002128.
 XX
 PR 02-JUN-1999; 99GB-00012852.

XX
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
DR WPI; 2001-071058/08.
XX
PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.
XX
PS Claim 7; Page 27; 63pp; English.
XX
CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVFPPF 15
|||||
Db 1 LKPFPKLKVEVFPPF 15

RESULT 3
AAB72253
ID AAB72253 standard; peptide; 15 AA.
XX
AC AAB72253;
XX
DT 14-MAY-2001 (first entry)
XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 8.
XX
KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
PN WO200111937-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US022818.
XX

PR 17-AUG-1999; 99US-0149311P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2001-202804/20.
 XX
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator.
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides
 CC have immune response modulatory activity, and are capable of inducing
 CC cytokines. Colostrinin and its derived peptides are useful for inducing
 CC cytokine production, for modulating an immunological response and for
 CC inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVFPPF 15
 |||||
 Db 1 LKPFPKLKVEVFPPF 15

RESULT 4
 AAB72539
 ID AAB72539 standard; peptide; 15 AA.
 XX
 AC AAB72539;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #8.
 XX
 KW Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX
 OS Unidentified.
 XX
 PN WO200112651-A2.
 XX
 PD 22-FEB-2001.

XX
 PF 17-AUG-2000; 2000WO-US022774.
 XX
 PR 17-AUG-1999; 99US-0149633P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I;
 XX
 DR WPI; 2001-226545/23.
 XX
 PT Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating damaged
 PT neural cells in a patient.
 XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPFPKPKLKEVFPPF 15
 |||||
 Db 1 LKPFPKPKLKEVFPPF 15

RESULT 5
 AAO14584

ID AAO14584 standard; peptide; 15 AA.
 XX
 AC AAO14584;
 XX
 DT 27-MAY-2002 (first entry)
 XX
 DE Neural cell regulatory colostrinin peptide 8.
 XX
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 15
 FT /note= "Optional C-terminal amide"
 XX
 PN WO200213851-A1.
 XX
 PD 21-FEB-2002.
 XX

PF 17-AUG-2000; 2000WO-US022777.
 XX
 PR 17-AUG-2000; 2000WO-US022777.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I, Stanton JG, Hughes TK;
 XX
 DR WPI; 2002-269152/31.
 XX
 PT Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 7; Page 21; 37pp; English.
 XX
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVFPPF 15
 |||||
 Db 1 LKPFPKLKVEVFPPF 15

RESULT 6

AAM51043

ID AAM51043 standard; peptide; 15 AA.

XX

AC AAM51043;

XX

DT 30-MAY-2002 (first entry)

XX

DE Colostrinin constituent peptide.

XX

KW Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 15

FT /note= "optional C-terminal amidation"

XX

PN WO200213849-A1.

XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022775.
XX
PR 17-AUG-2000; 2000WO-US022775.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
DR WPI; 2002-269150/31.
XX
PT Modulation of blood cell proliferation in a patient involves use of blood
PT cell regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX
PS Claim 1; Page 34; 54pp; English.
XX
CC The present sequence is that of a colostrinin constituent peptide that is
CC preferred for use as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. Methods are claimed for:
CC inducing a cytokine in a cell by contact with an immunological regulator,
CC where the cell is present in a cell culture, a tissue, an organ or an
CC organism, and the cell is mammalian, including human; modulating an
CC immune response in a cell by contact with the immunological regulator
CC under conditions effective to induce a cytokine; modulating an immune
CC response in a patient by administering an immunological regulator under
CC conditions effective to induce a cytokine, where the immunological
CC regulator is administered topically or as part of a dietary supplement,
CC and where the immune response is specific or non specific, an interferon
CC response or an antibody response; modulating blood cell proliferation by
CC contacting blood cells with a blood cell regulator, where the blood cells
CC are present in a cell culture or an organism, are mammalian or human, and
CC where the blood cells are increased in number or differentiated; and a
CC method for modulating blood cell proliferation in a patent. A claimed
CC cytokine-inducing composition comprises a pharmaceutical carrier and an
CC active agent such as the present peptide. Cytokines induced by this
CC peptide in human leucocyte cultures include interferon-gamma, tumour
CC necrosis factor-alpha, interleukin-6 and interleukin-10
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVFPPF 15
| | | | | | | | | | | | | | |
Db 1 LKPFPKLKVEVFPPF 15

RESULT 7
AAE20235
ID AAE20235 standard; peptide; 15 AA.
XX

AC AAE20235;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Colostrinin constituent peptide #8.
 XX
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnerary.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 15
 FT /note= "Optionally C-terminal amide"
 XX
 PN WO200213850-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022776.
 XX
 PR 17-AUG-2000; 2000WO-US022776.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2002-269151/31.
 XX
 PT Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog.
 XX
 PS Claim 6; Page 25; 51pp; English.
 XX
 CC The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress level
 CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
 CC organ, or organism; or for treating oxidative damage to the skin of a
 CC patient e.g. animal or human; to modulate oxidative stress during/ after
 CC a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVFPP 15
|||||||
Db 1 LKPFPKLKVEVFPP 15

RESULT 8

AAB59344

ID AAB59344 standard; peptide; 16 AA.

XX

AC AAB59344;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment derived sequence #4.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;

KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-071058/08.

XX

PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.

XX

PS Claim 8; Page 27; 63pp; English.

XX

CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques

XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 82; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVFPPF 15
| | | | | | | | | | | | | | | |
Db 2 LKPFPKLKVEVFPPF 16

RESULT 9

AAW48879

ID AAW48879 standard; peptide; 14 AA.

XX

AC AAW48879;

XX

DT 23-SEP-1998 (first entry)

XX

DE Cyclic peptide gramicidin S14 (GS14) analogue 3.

XX

KW Cyclic; gramicidin S14; GS; beta-pleated structure; therapeutic index;

KW hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;

KW mycoplasma; food additive; antimicrobial activity; GS14.

XX

OS Synthetic.

XX

PN WO9816549-A1.

XX

PD 23-APR-1998.

XX

PF 10-OCT-1997; 97WO-US018693.

XX

PR 11-OCT-1996; 96US-0028315P.

XX

PA (PENC-) PENCE INC.

PA (DEHL/) DEHLINGER P J.

XX

PI Kondejewski LH, Hodges RS, Wishart DS, Hancock REW, McElhaney R;

PI Prenner EJ, Lewis RNAH;

XX

DR WPI; 1998-251231/22.

XX

PT Cyclic peptide analogues of gramicidin S with broad spectrum

PT antimicrobial activity - and reduced haemolytic activity, have beta-

PT pleated sheet structure disrupted or eliminated by amino acid

PT substitutions.

XX

PS Claim 39; Page 65; 88pp; English.

XX

CC The invention provides for cyclic peptide analogues of gramicidin S14

CC (GS14; AAW48876) such as the present one. These cyclic peptide GS14

CC analogues do not have the beta-pleated structure present in GS as, for

CC e.g. residues 2, 4, 5 and 8-11 of the present cyclic peptide would be

CC substituted with the respective D-form residue. These analogues are

CC claimed to have an advantage over GS as they have broad spectrum

CC antimicrobial activity and an increased therapeutic index because they

CC lack the hemolytic effect of GS. The cyclic peptide GS14 analogues are

CC also claimed to be useful therapeutically in human or veterinary medicine

CC to kill or inhibit Gram-positive and Gram-negative bacteria, fungi and
CC mycoplasma. They may also be used to control mycoplasma contamination of
CC cultured cells and as food additives
XX
SQ Sequence 14 AA;

Query Match 45.7%; Score 37.5; DB 2; Length 14;
Best Local Similarity 69.2%; Pred. No. 15;
Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 LKPFPKLKVEVFP 13
|| || |||::||
Db 3 LKVFP-LKVKLFP 14

RESULT 10

AAW48904

ID AAW48904 standard; peptide; 14 AA.

XX

AC AAW48904;

XX

DT 23-SEP-1998 (first entry)

XX

DE Cyclic peptide gramicidin S14 analogue Y2/F2.

XX

KW Cyclic; gramicidin S; GS; beta-pleated structure; therapeutic index;

KW hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;

KW mycoplasma; food additive; antimicrobial activity.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1. .14

FT /note= "Residue 1 is in a peptide linkage with residue
FT 14"

FT Misc-difference 4

FT /note= "D-form residue"

FT Misc-difference 6

FT /note= "D-form residue"

FT Misc-difference 13

FT /note= "D-form residue"

XX

PN WO9816549-A1.

XX

PD 23-APR-1998.

XX

PF 10-OCT-1997; 97WO-US018693.

XX

PR 11-OCT-1996; 96US-0028315P.

XX

PA (PENC-) PENCE INC.

PA (DEHL/) DEHLINGER P J.

XX

PI Kondejewski LH, Hodges RS, Wishart DS, Hancock REW, McElhaney R;

PI Prenner EJ, Lewis RNAH;

XX

DR WPI; 1998-251231/22.

XX
PT Cyclic peptide analogues of gramicidin S with broad spectrum
PT antimicrobial activity - and reduced haemolytic activity, have beta-
PT pleated sheet structure disrupted or eliminated by amino acid
PT substitutions.
XX
PS Disclosure; Page 45; 88pp; English.
XX
CC The invention provides for cyclic peptide analogues of gramicidin S14
CC (GS14; AAW48876), such as the present one. These cyclic peptide GS14
CC analogues do not have the beta-pleated structure present in Gramicidin S
CC (GS). These analogues are claimed to have an advantage over GS as they
CC have broad spectrum antimicrobial activity and an increased therapeutic
CC index because they lack the hemolytic effect of GS. The cyclic peptide
CC GS14 analogues are also claimed to be useful therapeutically in human or
CC veterinary medicine to kill or inhibit Gram-positive and -negative
CC bacteria, fungi and mycoplasma. They may also be used to control
CC mycoplasma contamination of cultured cells and as food additives
XX
SQ Sequence 14 AA;

Query Match 45.7%; Score 37.5; DB 2; Length 14;
Best Local Similarity 69.2%; Pred. No. 15;
Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 LKPFPKLKVEVFP 13
|| || |||: ||
Db 3 LKVFP-LKVKLFP 14

RESULT 11
ABB41738
ID ABB41738 standard; peptide; 18 AA.
XX
AC ABB41738;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #9244 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.

XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 34373; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 18 AA;

Query Match 45.1%; Score 37; DB 4; Length 18;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KVEVFPPF 15
: || ||||
Db 3 RVEAFPPF 10

RESULT 12
AAM35535
ID AAM35535 standard; protein; 18 AA.
XX
AC AAM35535;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #9572 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488897/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 XX
 PS Claim 27; SEQ ID NO 35804; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP:
 CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders
 XX
 SQ Sequence 18 AA;

Query Match 45.1%; Score 37; DB 4; Length 18;
 Best Local Similarity 75.0%; Pred. No. 24;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 KVEVFPPF 15
 :|| ||||
 Db 3 RVEAFPPF 10

RESULT 13
 ABB25488

ID ABB25488 standard; protein; 18 AA.
 XX
 AC ABB25488;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Protein #7487 encoded by probe for measuring heart cell gene expression.
 XX
 KW Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200157274-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000666.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488899/53.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX
 PS Claim 15; SEQ ID NO 27258; 530pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 18 AA;

Query Match 45.1%; Score 37; DB 4; Length 18;
 Best Local Similarity 75.0%; Pred. No. 24;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KVEVFPPF 15
 :|| ||||
 Db 3 RVEAFPPF 10

RESULT 14

AAM75423

ID AAM75423 standard; protein; 18 AA.

XX

AC AAM75423;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 35729.

XX

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX

OS Homo sapiens.

XX

PN WO200157276-A2.

XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000668.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488900/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX
 PS Example 4; SEQ ID NO 35729; 658pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 XX
 SQ Sequence 18 AA;

Query Match 45.1%; Score 37; DB 4; Length 18;
 Best Local Similarity 75.0%; Pred. No. 24;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KVEVFPFP 15
 :|| ||||
 Db 3 RVEAFPPF 10

RESULT 15

AAM62611

ID AAM62611 standard; protein; 18 AA.

XX

AC AAM62611;

XX

DT 05-NOV-2001 (first entry)

XX

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 34716.

XX

KW Human; brain expressed exon; gene expression analysis; probe; microarray;

KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

XX

OS Homo sapiens.

XX

PN WO200157275-A2.
 XX
 PD. 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000667.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483446/52.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.
 XX
 PS Example 4; SEQ ID NO 34716; 650pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention
 XX
 SQ Sequence 18 AA;

 Query Match 45.1%; Score 37; DB 4; Length 18;
 Best Local Similarity 75.0%; Pred. No. 24;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 Qy 8 KVEVFPFP 15
 :|| ||||
 Db 3 RVEAFPPF 10

RESULT 16

ABG57176

ID ABG57176 standard; peptide; 18 AA.

XX

AC ABG57176;

XX

DT 25-FEB-2003 (first entry)

XX

DE Human liver peptide, SEQ ID No 35824.

XX

KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;

KW hypercholesterolaemia; coronary heart disease.

XX

OS Homo sapiens.
 XX
 PN WO200157273-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000664.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488898/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 XX
 PS Claim 27; SEQ ID NO 35824; 658pp; English.
 XX
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABG47348-ABG59930 represent human
 CC liver single exon encoded peptides of the invention. Note: The sequence
 CC information for this patent does not appear in the printed specification
 CC but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 18 AA;

Query Match 45.1%; Score 37; DB 4; Length 18;
 Best Local Similarity 75.0%; Pred. No. 24;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KVEVFPPF 15
 :|| ||||
 Db 3 RVEAFPPF 10

RESULT 17
 ABG45003
 ID ABG45003 standard; peptide; 18 AA.
 XX

AC ABG45003;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 34668.
 XX
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200186003-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000665.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2002-114183/15.
 XX
 PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX
 PS Claim 27; SEQ ID NO 34668; 634pp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC ; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably

CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 18 AA;

 Query Match 45.1%; Score 37; DB 5; Length 18;
 Best Local Similarity 75.0%; Pred. No. 24;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KVEVFPPF 15
 :|| ||||
 Db 3 RVEAFPPF 10

RESULT 18

AAB72520

ID AAB72520 standard; peptide; 18 AA.

XX

AC AAB72520;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #21.

XX

KW Dermatological; oxidative stress regulator; colostrinin.

XX

OS Unidentified.

XX

PN WO200112650-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022665.

XX

PR 17-AUG-1999; 99US-0149310P.

XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
DR WPI; 2001-218342/22.
XX
PT Modulating oxidative stress level in a cell, involves contacting the cell
PT with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations.
XX
PS Claim 6; Page 26; 48pp; English.
XX
CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient
XX
SQ Sequence 18 AA;

Query Match 43.9%; Score 36; DB 4; Length 18;
Best Local Similarity 70.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PFPKLVVEVF 12
| | | | |
Db 5 PFPKYPVEPF 14

RESULT 19

AAB59330

ID AAB59330 standard; peptide; 18 AA.

XX

AC AAB59330;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment C-5.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;

KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;
 XX
 DR WPI; 2001-071058/08.
 XX
 PT Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system and
 PT immune system, viral and bacterial infections, and diseases characterized
 PT by amyloid plaques.
 XX
 PS Claim 7; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques
 XX
 SQ Sequence 18 AA;

Query Match 43.9%; Score 36; DB 4; Length 18;
 Best Local Similarity 70.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PFPKLKVEVF 12
 |||| || |
 Db 5 PFPKYPVEPF 14

RESULT 20

AAB72267

ID AAB72267 standard; peptide; 18 AA.

XX

AC AAB72267;

XX

DT 14-MAY-2001 (first entry)

XX

DE Colostrinin derived cytokine inducing peptide SEQ ID 22.

XX

KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.

XX

OS Synthetic.

XX

PN WO200111937-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022818.

XX

PR 17-AUG-1999; 99US-0149311P.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2001-202804/20.
 XX
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator.
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides
 CC have immune response modulatory activity, and are capable of inducing
 CC cytokines. Colostrinin and its derived peptides are useful for inducing
 CC cytokine production, for modulating an immunological response and for
 CC inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies
 XX
 SQ Sequence 18 AA;

Query Match 43.9%; Score 36; DB 4; Length 18;
 Best Local Similarity 70.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PFPKLVVEVF 12
 |||| || |
 Db 5 PFPKYPVEPF 14

RESULT 21
 AAB72552
 ID AAB72552 standard; peptide; 18 AA.
 XX
 AC AAB72552;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #21.
 XX
 KW Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX
 OS Unidentified.
 XX
 PN WO200112651-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US022774.
 XX

PR 17-AUG-1999; 99US-0149633P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I;
 XX
 DR WPI; 2001-226545/23.
 XX
 PT Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating damaged
 PT neural cells in a patient.
 XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
 XX
 SQ Sequence 18 AA;

Query Match 43.9%; Score 36; DB 4; Length 18;
 Best Local Similarity 70.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PFPKLVKEVF 12
 |||| || |
 Db 5 PFPKYPVEPF 14

RESULT 22

AAO14598

ID AAO14598 standard; peptide; 18 AA.

XX

AC AAO14598;

XX

DT 27-MAY-2002 (first entry)

XX

DE Neural cell regulatory colostrinin peptide 21.

XX

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 18

FT /note= "Optional C-terminal amide"

XX

PN WO200213851-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022777.

XX

PR 17-AUG-2000; 2000WO-US022777.

XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Boldogh I, Stanton JG, Hughes TK;
XX
DR WPI; 2002-269152/31.
XX
PT Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX
PS Claim 7; Page 21; 37pp; English.
XX
CC The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention
XX
SQ Sequence 18 AA;

Query Match 43.9%; Score 36; DB 5; Length 18;
Best Local Similarity 70.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PFPKLKVEVF 12
| | | | | | |
Db 5 PFPKYPVEPF 14

RESULT 23

AAM51056

ID AAM51056 standard; peptide; 18 AA.

XX

AC AAM51056;

XX

DT 30-MAY-2002 (first entry)

XX

DE Colostrinin constituent peptide (casein amino acids 121-138).

XX

KW Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 18

FT /note= "optional C-terminal amidation"

XX

PN WO200213849-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022775.
 XX
 PR 17-AUG-2000; 2000WO-US022775.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2002-269150/31.
 XX
 PT Modulation of blood cell proliferation in a patient involves use of blood
 PT cell regulator selected from colostrinin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 1; Page 34; 54pp; English.
 XX
 CC The present sequence is that of a colostrinin constituent peptide that is
 CC preferred for use as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified as having
 CC a beta-casein homologue precursor, and corresponds to casein amino acids
 CC 121-138. Methods are claimed for: inducing a cytokine in a cell by
 CC contact with an immunological regulator, where the cell is present in a
 CC cell culture, a tissue, an organ or an organism, and the cell is
 CC mammalian, including human; modulating an immune response in a cell by
 CC contact with the immunological regulator under conditions effective to
 CC induce a cytokine; modulating an immune response in a patient by
 CC administering an immunological regulator under conditions effective to
 CC induce a cytokine, where the immunological regulator is administered
 CC topically or as part of a dietary supplement, and where the immune
 CC response is specific or non specific, an interferon response or an
 CC antibody response; modulating blood cell proliferation by contacting
 CC blood cells with a blood cell regulator, where the blood cells are
 CC present in a cell culture or an organism, are mammalian or human, and
 CC where the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A claimed
 CC cytokine-inducing composition comprises a pharmaceutical carrier and an
 CC active agent such as the present peptide. Cytokines induced by this
 CC peptide in human leucocyte cultures include interferon-gamma, tumour
 CC necrosis factor-alpha and interleukin-10
 XX
 SQ Sequence 18 AA;

Query Match 43.9%; Score 36; DB 5; Length 18;
 Best Local Similarity 70.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PFPKLVVEVF 12
 |||| || |
 Db 5 PFPKYPVEPF 14

RESULT 24
 AAE20249
 ID AAE20249 standard; peptide; 18 AA.
 XX
 AC AAE20249;

XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Colostrinin constituent peptide #21.
 XX
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnerary.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 18
 FT /note= "Optionally C-terminal amide"
 XX
 PN WO200213850-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022776.
 XX
 PR 17-AUG-2000; 2000WO-US022776.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2002-269151/31.
 XX
 PT Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog.
 XX
 PS Claim 6; Page 26; 51pp; English.
 XX
 CC The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress level
 CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
 CC organ, or organism; or for treating oxidative damage to the skin of a
 CC patient e.g. animal or human; to modulate oxidative stress during/ after
 CC a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide
 XX
 SQ Sequence 18 AA;

Query Match 43.9%; Score 36; DB 5; Length 18;
Best Local Similarity 70.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PFPKLKVEVF 12
|||| |||
Db 5 PFPKYPVEPF 14

RESULT 25

AAE07188

ID AAE07188 standard; peptide; 10 AA.

XX

AC AAE07188;

XX

DT 06-NOV-2001 (first entry)

XX

DE Colostrinin peptide 4.

XX

KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
KW central nervous system disorder; neurodegenerative disorder; weight loss;
KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
KW acquired immunological deficiency; neurological disorder; dementia;
KW antiviral.

XX

OS Unidentified.

XX

PN WO200155199-A1.

XX

PD 02-AUG-2001.

XX

PF 26-JAN-2001; 2001WO-GB000329.

XX

PR 26-JAN-2000; 2000GB-00001825.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-488775/53.

XX

PT Peptide useful as an interalia in the treatment of e.g. disorders of the
PT immune system and the central nervous system comprises ten amino-terminal
PT amino acid sequence derived from peptides present in colostrinin.

XX

PS Claim 1; Page 15; 40pp; English.

XX

CC The invention relates to colostrinin peptide fragments which are useful,
CC inter alia, in the treatment of chronic disorders of the immune system
CC and the central nervous system. Colostrinin peptides are used as a
CC medicament in the treatment of neurological disorders e.g., dementia,
CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
CC neurosis, in acquired immunological deficiencies, chronic bacterial and
CC viral infections and diseases characterised by the presence of beta-
CC amyloid plaques and as a dietary supplement for babies, small children,

CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxillary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child. The
 CC present sequence is colostrinin peptide 4 related to the invention
 XX
 SQ Sequence 10 AA;

Query Match 42.1%; Score 34.5; DB 4; Length 10;
 Best Local Similarity 81.8%; Pred. No. 33;
 Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 5 PKLKVEVFPPF 15
 ||||| | |
 Db 1 PKLKVEV-PEP 10

RESULT 26

AAE07198

ID AAE07198 standard; peptide; 11 AA.

XX

AC AAE07198;

XX

DT 06-NOV-2001 (first entry)

XX

DE Modified colostrinin cyclic peptide #4.

XX

KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral; cyclic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl; this residue forms a cyclic
 FT linkage with Pro found at the C-terminal end"

XX

PN WO200155199-A1.

XX

PD 02-AUG-2001.

XX

PF 26-JAN-2001; 2001WO-GB000329.

XX

PR 26-JAN-2000; 2000GB-00001825.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX
 DR WPI; 2001-488775/53.
 XX
 PT Peptide useful as an inter alia in the treatment of e.g. disorders of the
 PT immune system and the central nervous system comprises ten amino-terminal
 PT amino acid sequence derived from peptides present in colostrinin.
 XX
 PS Example 2; Page 8; 40pp; English.
 XX
 CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxillary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child. The
 CC present sequence is modified colostrinin cyclic peptide #4 related to the
 CC invention
 XX
 SQ Sequence 11 AA;

Query Match 42.1%; Score 34.5; DB 4; Length 11;
 Best Local Similarity 81.8%; Pred. No. 37;
 Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 5 PKLKVEVPFP 15
 ||||| | |
 Db 2 PKLKVEV-PEP 11

RESULT 27

AAW48877

ID AAW48877 standard; peptide; 14 AA.

XX

AC AAW48877;

XX

DT 23-SEP-1998 (first entry)

XX

DE Cyclic peptide gramicidin S14 (GS14) analogue 1.

XX

KW Cyclic; gramicidin S14; GS; beta-pleated structure; therapeutic index;

KW hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;

KW mycoplasma; food additive; antimicrobial activity; GS14.

XX

OS Synthetic.

XX

FH	Key	Location/Qualifiers
FT	Misc-difference 1.	.14
FT		/note= "Residue 1 is in a peptide linkage with residue
FT		14"
FT	Misc-difference 2	
FT		/note= "Optionally D-form residue"
FT	Misc-difference 4	
FT		/note= "Optionally D-form residue"
FT	Misc-difference 5	
FT		/note= "Optionally D-form residue"
FT	Misc-difference 6	
FT		/note= "D-form residue"
FT	Misc-difference 8	
FT		/note= "Optionally D-form residue"
FT	Misc-difference 9	
FT		/note= "Optionally D-form residue"
FT	Misc-difference 10	
FT		/note= "Optionally D-form residue"
FT	Misc-difference 11	
FT		/note= "Optionally D-form residue"
FT	Misc-difference 13	
FT		/note= "D-form residue"
XX		
PN	WO9816549-A1.	
XX		
PD	23-APR-1998.	
XX		
PF	10-OCT-1997;	97WO-US018693.
XX		
PR	11-OCT-1996;	96US-0028315P.
XX		
PA	(PENC-) PENCE INC.	
PA	(DEHL/) DEHLINGER P J.	
XX		
PI	Kondejewski LH, Hodges RS, Wishart DS, Hancock REW, Mcelhaney R;	
PI	Prenner EJ, Lewis RNAH;	
XX		
DR	WPI; 1998-251231/22.	
XX		
PT	Cyclic peptide analogues of gramicidin S with broad spectrum	
PT	antimicrobial activity - and reduced haemolytic activity, have beta-	
PT	pleated sheet structure disrupted or eliminated by amino acid	
PT	substitutions.	
XX		
PS	Claim 39; Page 65; 88pp; English.	
XX		
CC	The invention provides for cyclic peptide analogues of gramicidin S14	
CC	(GS14; AAW48876) such as the present one. These cyclic peptide GS14	
CC	analogues do not have the beta-pleated structure present in GS as, for	
CC	e.g. residues 2, 4, 5 and 8-11 of the present cyclic peptide would be	
CC	substituted with the respective D-form residue. These analogues are	
CC	claimed to have an advantage over GS as they have broad spectrum	
CC	antimicrobial activity and an increased therapeutic index because they	
CC	lack the hemolytic effect of GS. The cyclic peptide GS14 analogues are	
CC	also claimed to be useful therapeutically in human or veterinary medicine	
CC	to kill or inhibit Gram-positive and Gram-negative bacteria, fungi and	
CC	mycoplasma. They may also be used to control mycoplasma contamination of	

CC cultured cells and as food additives
XX
SQ Sequence 14 AA;

Query Match 42.1%; Score 34.5; DB 2; Length 14;
Best Local Similarity 61.5%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 LKPFPKLKVEVFP 13
|| || |||:::|
Db 3 LKVFP-LKVKLYP 14

RESULT 28

AAW48878

ID AAW48878 standard; peptide; 14 AA.

XX

AC AAW48878;

XX

DT 23-SEP-1998 (first entry)

XX

DE Cyclic peptide gramicidin S14 (GS14) analogue 2.

XX

KW Cyclic; gramicidin S14; GS; beta-pleated structure; therapeutic index;

KW hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;

KW mycoplasma; food additive; antimicrobial activity; GS14.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1. .14

FT /note= "Residue 1 is in a peptide linkage with residue
14"

FT Misc-difference 2

FT /note= "Optionally D-form residue"

FT Misc-difference 4

FT /note= "Optionally D-form residue"

FT Misc-difference 5

FT /note= "Optionally D-form residue"

FT Misc-difference 6

FT /note= "D-form residue"

FT Misc-difference 8

FT /note= "Optionally D-form residue"

FT Misc-difference 9

FT /note= "Optionally D-form residue"

FT Misc-difference 10

FT /note= "Optionally D-form residue"

FT Misc-difference 11

FT /note= "Optionally D-form residue"

FT Misc-difference 13

FT /note= "D-form residue"

XX

PN WO9816549-A1.

XX

PD 23-APR-1998.

XX

PF 10-OCT-1997; 97WO-US018693.

XX
 PR 11-OCT-1996; 96US-0028315P.
 XX
 PA (PENC-) PENCE INC.
 PA (DEHL/) DEHLINGER P J.
 XX
 PI Kondejewski LH, Hodges RS, Wishart DS, Hancock REW, Mcelhaney R;
 PI Prenner EJ, Lewis RNAH;
 XX
 DR WPI; 1998-251231/22.
 XX
 PT Cyclic peptide analogues of gramicidin S with broad spectrum
 PT antimicrobial activity - and reduced haemolytic activity, have beta-
 PT pleated sheet structure disrupted or eliminated by amino acid
 PT substitutions.
 XX
 PS Claim 39; Page 65; 88pp; English.
 XX
 CC The invention provides for cyclic peptide analogues of gramicidin S14
 CC (GS14; AAW48876) such as the present one. These cyclic peptide GS14
 CC analogues do not have the beta-pleated structure present in GS as, for
 CC e.g. residues 2, 4, 5 and 8-11 of the present cyclic peptide would be
 CC substituted with the respective D-form residue. These analogues are
 CC claimed to have an advantage over GS as they have broad spectrum
 CC antimicrobial activity and an increased therapeutic index because they
 CC lack the hemolytic effect of GS. The cyclic peptide GS14 analogues are
 CC also claimed to be useful therapeutically in human or veterinary medicine
 CC to kill or inhibit Gram-positive and Gram-negative bacteria, fungi and
 CC mycoplasma. They may also be used to control mycoplasma contamination of
 CC cultured cells and as food additives
 XX
 SQ Sequence 14 AA;

Query Match 42.1%; Score 34.5; DB 2; Length 14;
 Best Local Similarity 61.5%; Pred. No. 48;
 Matches 8; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 LKPFPKLKVEVFP 13
 || :| |||::||
 Db 3 LKVYP-LKVKLFP 14

RESULT 29

AAE07187

ID AAE07187 standard; peptide; 10 AA.

XX

AC AAE07187;

XX

DT 06-NOV-2001 (first entry)

XX

DE Colostrinin peptide 3.

XX

KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;

KW antiviral.
 XX
 OS Unidentified.
 XX
 PN WO200155199-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-GB000329.
 XX
 PR 26-JAN-2000; 2000GB-00001825.
 XX
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Georgiades JA;
 XX
 DR WPI; 2001-488775/53.
 XX
 PT Peptide useful as an inter alia in the treatment of e.g. disorders of the
 PT immune system and the central nervous system comprises ten amino-terminal
 PT amino acid sequence derived from peptides present in colostrinin.
 XX
 PS Claim 1; Page 15; 40pp; English.
 XX
 CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxillary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child. The
 CC present sequence is colostrinin peptide 3 related to the invention
 XX
 SQ Sequence 10 AA;

Query Match 41.5%; Score 34; DB 4; Length 10;
 Best Local Similarity 70.0%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEVFPF 14
 | | | |
 Db 1 PVLPEVFPF 10

RESULT 30
 AAB72504

ID AAB72504 standard; peptide; 15 AA.
 XX
 AC AAB72504;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #5.
 XX
 KW Dermatological; oxidative stress regulator; colostrinin.
 XX
 OS Unidentified.
 XX
 PN WO200112650-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US022665.
 XX
 PR 17-AUG-1999; 99US-0149310P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2001-218342/22.
 XX
 PT Modulating oxidative stress level in a cell, involves contacting the cell
 PT with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations.
 XX
 PS Claim 6; Page 25; 48pp; English.
 XX
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient
 XX
 SQ Sequence 15 AA;

Query Match 41.5%; Score 34; DB 4; Length 15;
 Best Local Similarity 70.0%; Pred. No. 62;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEVFPF 14
 | | | | |
 Db 5 PVLPEVFPF 14

RESULT 31

AAB59322

ID AAB59322 standard; peptide; 15 AA.
 XX
 AC AAB59322;
 XX

DT 21-MAR-2001 (first entry)
 XX
 DE Ewe colostrinin peptide fragment B-7.
 XX
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 OS Ovis sp.
 XX
 PN WO200075173-A2.
 XX
 PD 14-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-GB002128.
 XX
 PR 02-JUN-1999; 99GB-00012852.
 XX
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Georgiades JA;
 XX
 DR WPI; 2001-071058/08.
 XX
 PT Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system and
 PT immune system, viral and bacterial infections, and diseases characterized
 PT by amyloid plaques.
 XX
 PS Claim 7; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques
 XX
 SQ Sequence 15 AA;

Query Match 41.5%; Score 34; DB 4; Length 15;
 Best Local Similarity 70.0%; Pred. No. 62;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEVFPF 14
 | | | |
 Db 5 PVLPVEPFPF 14

RESULT 32
 AAB72250
 ID AAB72250 standard; peptide; 15 AA.
 XX
 AC AAB72250;
 XX
 DT 14-MAY-2001 (first entry)

XX
 DE Colostrinin derived cytokine inducing peptide SEQ ID 5.
 XX
 KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX
 OS Synthetic.
 XX
 PN WO200111937-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US022818.
 XX
 PR 17-AUG-1999; 99US-0149311P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2001-202804/20.
 XX
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator.
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides
 CC have immune response modulatory activity, and are capable of inducing
 CC cytokines. Colostrinin and its derived peptides are useful for inducing
 CC cytokine production, for modulating an immunological response and for
 CC inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies
 XX
 SQ Sequence 15 AA;

 Query Match 41.5%; Score 34; DB 4; Length 15;
 Best Local Similarity 70.0%; Pred. No. 62;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 Qy 5 PKLKVEVFPP 14
 | | || ||
 Db 5 PVLPEVFPP 14

 RESULT 33
 AAB72536

ID AAB72536 standard; peptide; 15 AA.
 XX
 AC AAB72536;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #5.
 XX
 KW Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX
 OS Unidentified.
 XX
 PN WO200112651-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US022774.
 XX
 PR 17-AUG-1999; 99US-0149633P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I;
 XX
 DR WPI; 2001-226545/23.
 XX
 PT Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating damaged
 PT neural cells in a patient.
 XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
 XX
 SQ Sequence 15 AA;

Query Match 41.5%; Score 34; DB 4; Length 15;
 Best Local Similarity 70.0%; Pred. No. 62;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEVFPPF 14
 | | || ||
 Db 5 PVLPEVFPPF 14

RESULT 34
 AA014581
 ID AA014581 standard; peptide; 15 AA.
 XX
 AC AA014581;
 XX
 DT 27-MAY-2002 (first entry)
 XX

DE Neural cell regulatory colostrinin peptide 5.
 XX
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 15
 FT /note= "Optional C-terminal amide"
 XX
 PN WO200213851-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022777.
 XX
 PR 17-AUG-2000; 2000WO-US022777.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I, Stanton JG, Hughes TK;
 XX
 DR WPI; 2002-269152/31.
 XX
 PT Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 7; Page 21; 37pp; English.
 XX
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention
 XX
 SQ Sequence 15 AA;

Query Match 41.5%; Score 34; DB 5; Length 15;
 Best Local Similarity 70.0%; Pred. No. 62;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEVFPP 14
 | | | | |
 Db 5 PVLPEVFPP 14

RESULT 35
 AAM51040
 ID AAM51040 standard; peptide; 15 AA.
 XX

AC AAM51040;
 XX
 DT 30-MAY-2002 (first entry)
 XX
 DE Colostrinin constituent peptide.
 XX
 KW Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 15
 FT /note= "optional C-terminal amidation"
 XX
 PN WO200213849-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022775.
 XX
 PR 17-AUG-2000; 2000WO-US022775.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2002-269150/31.
 XX
 PT Modulation of blood cell proliferation in a patient involves use of blood
 PT cell regulator selected from colostrinin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 1; Page 34; 54pp; English.
 XX
 CC The present sequence is that of a colostrinin constituent peptide that is
 CC preferred for use as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified as having
 CC a beta-casein homologue precursor. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator, where the
 CC cell is present in a cell culture, a tissue, an organ or an organism, and
 CC the cell is mammalian, including human; modulating an immune response in
 CC a cell by contact with the immunological regulator under conditions
 CC effective to induce a cytokine; modulating an immune response in a
 CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator is
 CC administered topically or as part of a dietary supplement, and where the
 CC immune response is specific or non specific, an interferon response or an
 CC antibody response; modulating blood cell proliferation by contacting
 CC blood cells with a blood cell regulator, where the blood cells are
 CC present in a cell culture or an organism, are mammalian or human, and
 CC where the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A claimed
 CC cytokine-inducing composition comprises a pharmaceutical carrier and an
 CC active agent such as the present peptide. Cytokines induced by this
 CC peptide in human leucocyte cultures include interferon-gamma, tumour

CC necrosis factor-alpha, interleukin-6 and interleukin-10
XX
SQ Sequence 15 AA;

Query Match 41.5%; Score 34; DB 5; Length 15;
Best Local Similarity 70.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEVFPPF 14
| | || |||
Db 5 PVLPEVFPPF 14

RESULT 36

AAE20232

ID AAE20232 standard; peptide; 15 AA.

XX

AC AAE20232;

XX

DT 18-JUN-2002 (first entry)

XX

DE Colostrinin constituent peptide #5.

XX

KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnerary.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 15

FT /note= "Optionally C-terminal amide"

XX

PN WO200213850-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022776.

XX

PR 17-AUG-2000; 2000WO-US022776.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Stanton GJ, Hughes TK, Boldogh I;

XX

DR WPI; 2002-269151/31.

XX

PT Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog.

XX

PS Claim 6; Page 25; 5lpp; English.

XX

CC The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress level

CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
 CC organ, or organism; or for treating oxidative damage to the skin of a
 CC patient e.g. animal or human; to modulate oxidative stress during/ after
 CC a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide
 XX
 SQ Sequence 15 AA;

Query Match 41.5%; Score 34; DB 5; Length 15;
 Best Local Similarity 70.0%; Pred. No. 62;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEVFPP 14
 | | | | |
 Db 5 PVLPEVFPP 14

RESULT 37

AAB59352

ID AAB59352 standard; peptide; 16 AA.

XX

AC AAB59352;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment derived sequence #12.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-071058/08.

XX

PT Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.

XX

PS Claim 8; Page 27; 63pp; English.

XX

CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques

XX

SQ Sequence 16 AA;

Query Match 41.5%; Score 34; DB 4; Length 16;
Best Local Similarity 70.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEVFPP 14

| | || ||

Db 6 PVLPVEVFPP 15

RESULT 38

AAW48905

ID AAW48905 standard; peptide; 14 AA.

XX

AC AAW48905;

XX

DT 23-SEP-1998 (first entry)

XX

DE Cyclic peptide gramicidin S14 analogue Y2/F2 V3/L3.

XX

KW Cyclic; gramicidin S; GS; beta-pleated structure; therapeutic index;
KW hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;
KW mycoplasma; food additive; antimicrobial activity.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1. .14

FT /note= "Residue 1 is in a peptide linkage with residue
FT 14"

FT Misc-difference 4

FT /note= "D-form residue"

FT Misc-difference 6

FT /note= "D-form residue"

FT Misc-difference 13

FT /note= "D-form residue"

XX

PN WO9816549-A1.

XX

PD 23-APR-1998.

XX

PF 10-OCT-1997; 97WO-US018693.
 XX
 PR 11-OCT-1996; 96US-0028315P.
 XX
 PA (PENC-) PENCE INC.
 PA (DEHL/) DEHLINGER P J.
 XX
 PI Kondejewski LH, Hodges RS, Wishart DS, Hancock REW, Mcelhaney R;
 PI Prenner EJ, Lewis RNAH;
 XX
 DR WPI; 1998-251231/22.
 XX
 PT Cyclic peptide analogues of gramicidin S with broad spectrum
 PT antimicrobial activity - and reduced haemolytic activity, have beta-
 PT pleated sheet structure disrupted or eliminated by amino acid
 PT substitutions.
 XX
 PS Disclosure; Page 45; 88pp; English.
 XX
 CC The invention provides for cyclic peptide analogues of gramicidin S14
 CC (GS14; AAW48876), such as the present one. These cyclic peptide GS14
 CC analogues do not have the beta-pleated structure present in Gramicidin S
 CC (GS). These analogues are claimed to have an advantage over GS as they
 CC have broad spectrum antimicrobial activity and an increased therapeutic
 CC index because they lack the hemolytic effect of GS. The cyclic peptide
 CC GS14 analogues are also claimed to be useful therapeutically in human or
 CC veterinary medicine to kill or inhibit Gram-positive and -negative
 CC bacteria, fungi and mycoplasma. They may also be used to control
 CC mycoplasma contamination of cultured cells and as food additives
 XX
 SQ Sequence 14 AA;

Query Match 40.9%; Score 33.5; DB 2; Length 14;
 Best Local Similarity 61.5%; Pred. No. 70;
 Matches 8; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 LKPFPKLKVEVFP 13
 || || ||::||
 Db 3 LKLFP-LKLKLFP 14

RESULT 39

AAR58339

ID AAR58339 standard; peptide; 14 AA.

XX

AC AAR58339;

XX

DT 22-SEP-1994 (first entry)

XX

DE Hypotensive polypeptide.

XX

KW Hypotensive; antioxidative; calcium absorption; salt; food;

KW pharmaceuticals; physiologically active agents.

XX

OS Lactobacillus helveticus.

XX

PN JP06041191-A.

XX
 PD 15-FEB-1994.
 XX
 PF 03-MAR-1993; 93JP-00043047.
 XX
 PR 04-MAR-1992; 92JP-00047340.
 XX
 PA (CALV) CALPIS SHOKUHHIN KOGYO KK.
 XX
 DR WPI; 1994-089332/11.
 XX
 PT New polypeptide - used in physiologically active agents having e.g.
 PT hypotensive antioxidative and calcium absorption promoting activity.
 XX
 PS Claim 1-2; Page 10; 10pp; Japanese.
 XX
 CC Sequences (AAR58319-341) are used in conjunction with physiologically
 CC active agents showing a property such as hypotensive activity, calcium
 CC absorption promoting activity and antioxidative activity. The peptides are
 CC non-toxic and can be used in physiologically active agents
 XX
 SQ Sequence 14 AA;

Query Match 40.2%; Score 33; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 85;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PFPKLKVEVF 12
 |||| | : |
 Db 5 PFPKYPVQPF 14

RESULT 40

AAW48906

ID AAW48906 standard; peptide; 14 AA.

XX

AC AAW48906;

XX

DT 23-SEP-1998 (first entry)

XX

DE Cyclic peptide gramicidin S14 analogue GS14napol.

XX

KW Cyclic; gramicidin S; GS; beta-pleated structure; therapeutic index;

KW hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi;

KW mycoplasma; food additive; antimicrobial activity; GS14napol.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1. .14

FT /note= "Residue 1 is in a peptide linkage with residue
14"

FT Misc-difference 6

FT /note= "D-form residue"

FT Misc-difference 13

FT /note= "D-form residue"

XX

PN WO9816549-A1.
 XX
 PD 23-APR-1998.
 XX
 PF 10-OCT-1997; 97WO-US018693.
 XX
 PR 11-OCT-1996; 96US-0028315P.
 XX
 PA (PENC-) PENCE INC.
 PA (DEHL/) DEHLINGER P J.
 XX
 PI Kondejewski LH, Hodges RS, Wishart DS, Hancock REW, Mcelhaney R;
 PI Prenner EJ, Lewis RNAH;
 XX
 DR WPI; 1998-251231/22.
 XX
 PT Cyclic peptide analogues of gramicidin S with broad spectrum
 PT antimicrobial activity - and reduced haemolytic activity, have beta-
 PT pleated sheet structure disrupted or eliminated by amino acid
 PT substitutions.
 XX
 PS Disclosure; Page 48; 88pp; English.
 XX
 CC The invention provides for cyclic peptide analogues of gramicidin S14
 CC (GS14; AAW48876), such as the present cyclic GS14 polarized non-
 CC amphipathic (GS14napol) peptide. These cyclic peptide GS14 analogues do
 CC not have the beta-pleated structure present in Gramicidin S (GS). These
 CC analogues are claimed to have an advantage over GS as they have broad
 CC spectrum antimicrobial activity and an increased therapeutic index
 CC because they lack the hemolytic effect of GS. The cyclic peptide GS14
 CC analogues are also claimed to be useful therapeutically in human or
 CC veterinary medicine to kill or inhibit Gram-positive and -negative
 CC bacteria, fungi and mycoplasma. They may also be used to control
 CC mycoplasma contamination of cultured cells and as food additives
 XX
 SQ Sequence 14 AA;

 Query Match 39.6%; Score 32.5; DB 2; Length 14;
 Best Local Similarity 61.5%; Pred. No. 1e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

 Qy 1 LKPFPKLKVEVFP 13
 ||:|| || |:|
 Db 3 LKKYPK-KVLVYP 14

 RESULT 41
 ABJ01855
 ID ABJ01855 standard; peptide; 9 AA.
 XX
 AC ABJ01855;
 XX
 DT 19-SEP-2002 (first entry)
 XX
 DE 158P1D7 related HLA peptide SEQ ID No 555.
 XX
 KW Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;

KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
 KW HLA.
 XX
 OS Homo sapiens.
 XX
 PN WO200216593-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 22-AUG-2001; 2001WO-US026276.
 XX
 PR 22-AUG-2000; 2000US-0227098P.
 PR 10-APR-2001; 2001US-0282739P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
 PI Challita-Eid PM, Jakobovits A;
 XX
 DR WPI; 2002-425659/45.
 XX
 PT New compositions comprising a gene (designated 158P1D7), its encoded
 PT protein or their modulators, useful for treating or diagnosing cancers,
 PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses or
 PT humans).
 XX
 PS Disclosure; Page 146; 181pp; English.
 XX
 CC The invention relates to a novel nucleic acid, designated 158P1D7. The
 CC compositions are useful for treating or diagnosing cancers, particularly
 CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
 CC horses or humans). The compositions are also useful for monitoring
 CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
 CC of the invention can be used in gene therapy to treat the said disorders.
 CC This sequence represents a human leukocyte antigen (HLA) peptide relating
 CC to the 158P1D7 protein of the invention
 XX
 SQ Sequence 9 AA;

Query Match 39.0%; Score 32; DB 5; Length 9;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PFPKLVK 9
 | |||||
 Db 2 PMPKLVK 8

RESULT 42
 ABJ01751
 ID ABJ01751 standard; peptide; 9 AA.
 XX
 AC ABJ01751;
 XX
 DT 19-SEP-2002 (first entry)
 XX
 DE 158P1D7 related HLA peptide SEQ ID No 451.

XX
 KW Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
 KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
 KW HLA.
 XX
 OS Homo sapiens.
 XX
 PN WO200216593-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 22-AUG-2001; 2001WO-US026276.
 XX
 PR 22-AUG-2000; 2000US-0227098P.
 PR 10-APR-2001; 2001US-0282739P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
 PI Challita-Eid PM, Jakobovits A;
 XX
 DR WPI; 2002-425659/45.
 XX
 PT New compositions comprising a gene (designated 158P1D7), its encoded
 PT protein or their modulators, useful for treating or diagnosing cancers,
 PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses or
 PT humans).
 XX
 PS Disclosure; Page 142; 181pp; English.
 XX
 CC The invention relates to a novel nucleic acid, designated 158P1D7. The
 CC compositions are useful for treating or diagnosing cancers, particularly
 CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
 CC horses or humans). The compositions are also useful for monitoring
 CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
 CC of the invention can be used in gene therapy to treat the said disorders.
 CC This sequence represents a human leukocyte antigen (HLA) peptide relating
 CC to the 158P1D7 protein of the invention
 XX
 SQ Sequence 9 AA;

Query Match 39.0%; Score 32; DB 5; Length 9;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLKV 9
 | |||||
 Db 2 PMPKLKV 8

RESULT 43
 ABJ01996
 ID ABJ01996 standard; peptide; 9 AA.
 XX
 AC ABJ01996;
 XX
 DT 19-SEP-2002 (first entry)

XX
DE 158P1D7 related HLA peptide #37.
XX
KW Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW HLA.
XX
OS Homo sapiens.
XX
PN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-US026276.
XX
PR 22-AUG-2000; 2000US-0227098P.
PR 10-APR-2001; 2001US-0282739P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Challita-Eid PM, Jakobovits A;
XX
DR WPI; 2002-425659/45.
XX
PT New compositions comprising a gene (designated 158P1D7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses or
PT humans).
XX
PS Disclosure; Page 140; 181pp; English.
XX
CC The invention relates to a novel nucleic acid, designated 158P1D7. The
CC compositions are useful for treating or diagnosing cancers, particularly
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158P1D7 protein of the invention
XX
SQ Sequence 9 AA;

Query Match 39.0%; Score 32; DB 5; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLV 9
| | | | |
Db 2 PMPKLV 8

RESULT 44
ABJ01907
ID ABJ01907 standard; peptide; 10 AA.
XX
AC ABJ01907;

XX
 DT 19-SEP-2002 (first entry)
 XX
 DE 158P1D7 related HLA peptide SEQ ID No 607.
 XX
 KW Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
 KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
 KW HLA.
 XX
 OS Homo sapiens.
 XX
 PN WO200216593-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 22-AUG-2001; 2001WO-US026276.
 XX
 PR 22-AUG-2000; 2000US-0227098P.
 PR 10-APR-2001; 2001US-0282739P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
 PI Challita-Eid PM, Jakobovits A;
 XX
 DR WPI; 2002-425659/45.
 XX
 PT New compositions comprising a gene (designated 158P1D7), its encoded
 PT protein or their modulators, useful for treating or diagnosing cancers,
 PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses or
 PT humans).
 XX
 PS Disclosure; Page 147; 181pp; English.
 XX
 CC The invention relates to a novel nucleic acid, designated 158P1D7. The
 CC compositions are useful for treating or diagnosing cancers, particularly
 CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
 CC horses or humans). The compositions are also useful for monitoring
 CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
 CC of the invention can be used in gene therapy to treat the said disorders.
 CC This sequence represents a human leukocyte antigen (HLA) peptide relating
 CC to the 158P1D7 protein of the invention
 XX
 SQ Sequence 10 AA;

Query Match 39.0%; Score 32; DB 5; Length 10;
 Best Local Similarity 85.7%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLKV 9
 | |||||
 Db 2 PMPKLKV 8

RESULT 45
 ABJ01366
 ID ABJ01366 standard; peptide; 10 AA.

XX
 AC ABJ01366;
 XX
 DT 19-SEP-2002 (first entry)
 XX
 DE 158P1D7 related HLA peptide SEQ ID No 66.
 XX
 KW Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
 KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
 KW HLA.
 XX
 OS Homo sapiens.
 XX
 PN WO200216593-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 22-AUG-2001; 2001WO-US026276.
 XX
 PR 22-AUG-2000; 2000US-0227098P.
 PR 10-APR-2001; 2001US-0282739P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
 PI Challita-Eid PM, Jakobovits A;
 XX
 DR WPI; 2002-425659/45.
 XX
 PT New compositions comprising a gene (designated 158P1D7), its encoded
 PT protein or their modulators, useful for treating or diagnosing cancers,
 PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses or
 PT humans).
 XX
 PS Disclosure; Page 128; 181pp; English.
 XX
 CC The invention relates to a novel nucleic acid, designated 158P1D7. The
 CC compositions are useful for treating or diagnosing cancers, particularly
 CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
 CC horses or humans). The compositions are also useful for monitoring
 CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
 CC of the invention can be used in gene therapy to treat the said disorders.
 CC This sequence represents a human leukocyte antigen (HLA) peptide relating
 CC to the 158P1D7 protein of the invention
 XX
 SQ Sequence 10 AA;

Query Match 39.0%; Score 32; DB 5; Length 10;
 Best Local Similarity 85.7%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PFPKLKV 9
 | |||||
 Db 2 PMPKLKV 8

RESULT 46

AAW38528

ID AAW38528 standard; protein; 16 AA.

XX

AC AAW38528;

XX

DT 06-NOV-1998 (first entry)

XX

DE *S. pneumoniae* methylene tetrahydrofolate reductase.

XX

KW *Streptococcus pneumoniae* protein; genetic immunisation; antagonist;
KW immunological response; inoculation; antibody production; inhibitor;
KW T cell immune response; antimicrobial compound; bacterial adhesion;
KW extracellular matrix protein; protein-mediated cell invasion; wound;
KW pathogenesis.

XX

OS *Streptococcus pneumoniae*.

XX

PN WO9743303-A1.

XX

PD 20-NOV-1997.

XX

PF 14-MAY-1997; 97WO-US007950.

XX

PR 14-MAY-1996; 96US-0017670P.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Black MT, Hodgson JE, Knowles DJC, Nicholas RO, Stodola RK;

XX

DR WPI; 1998-008793/01.

DR N-PSDB; AAT98588.

XX

PT Novel *Streptococcus pneumoniae* proteins and related DNA - useful for
PT diagnosing anti-microbial agents for treatment of bacterial infections.

XX

PS Claim 12; Page 308; 483pp; English.

XX

CC This sequence represents a *Streptococcus pneumoniae* protein that, based
CC on homology with *S. typhimurium* protein, is a methylene tetrahydrofolate
CC reductase, and is encoded by a DNA sequence of the invention. The DNA
CC sequences were isolated from *Streptococcus pneumoniae* strain 0100993
CC (NCIMB 40794). The *Streptococcus pneumoniae* proteins of the invention can
CC be used to identify compounds which interact with and inhibit or activate
CC the activity of the proteins. Antagonists can be used to treat diseases
CC caused by *S. pneumoniae* proteins, through genetic immunisation. They can
CC also be used to induce an immunological response in a mammal by
CC inoculation with the *S. pneumoniae* proteins or delivery of the encoding
CC nucleic acids in a vector adequate to produce antibody and/or T cell
CC immune responses to protect the animal from disease. The proteins can
CC also be used to identify antimicrobial compounds which are capable of
CC inhibiting their bioactivity. In particular the proteins of the invention
CC can be used to prevent adhesion of bacteria to mammalian extracellular
CC matrix proteins on in-dwelling devices or in wounds, to block protein-
CC mediated mammalian cell invasion, and to block the normal progression of
CC pathogenesis in infections initiated other than by the implantation of in
CC -dwelling devices or other surgical techniques

XX

SQ Sequence 16 AA;

Query Match 39.0%; Score 32; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEVFP 13
| | |||
Db 6 PSLSFEVFP 14

RESULT 47

ABB77148

ID ABB77148 standard; peptide; 16 AA.

XX

AC ABB77148;

XX

DT 15-JUL-2002 (first entry)

XX

DE Classical swine fever virus envelope protein E2 epitope #20.

XX

KW Classisical swine fever virus; envelope protein; E2; vaccine; virucide;
pig.

XX

OS Classical swine fever virus.

XX

PN WO200220048-A1.

XX

PD 14-MAR-2002.

XX

PF 20-JUL-2001; 2001WO-CN001189.

XX

PR 10-AUG-2000; 2000CN-00121292.

XX

PA (UYQI) UNIV QINGHUA.

PA (BEIJ-) BEIJING FEIKAI BIOTECH CO LTD.

XX

PI Chen Y, Dong X, Xiao Y;

XX

DR WPI; 2002-292232/33.

XX

PT Production of classical swine fever virus epitope vaccines containing
PT conjugated epitope peptides, useful in treating mutation of classical
PT swine fever virus particularly applicable in pig farming.

XX

PS Claim 5; Page 8; 13pp; Chinese.

XX

CC The sequence represents an epitope of the classical swine fever virus
CC envelope protein E2. The invention relates to a novel classical swine
CC fever virus vaccine comprising at least 1 epitope peptide conjugated to a
CC carrier protein or peptide and each having mono-epitopes repeated at
CC least once or multi-epitopes repeated at least once, in which the
CC epitopes are chosen from neutralizing epitope on envelope protein E2 of
CC classical swine fever virus and mutation epitope. The vaccine of the
CC invention has virucide activity. The vaccines are useful in treating
CC mutation of classical swine fever virus and curing the fever, and are

CC particularly applicable in pig farming
XX
SQ Sequence 16 AA;

Query Match 39.0%; Score 32; DB 5; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KPFPKLVKVEVFP 13
|||| : : ||
Db 4 KPFPKLVKVEVFP 15

RESULT 48

ABP82437

ID ABP82437 standard; peptide; 16 AA.

XX

AC ABP82437;

XX

DT 04-MAR-2003 (first entry)

XX

DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1110.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

KW G protein-coupled receptor modulator; antibody; immune-related disease;

KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

KW immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

KW ulcer.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US050107.

XX

PR 19-DEC-2000; 2000US-0257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burmer GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors

PT (GPCR), useful for diagnosing and designing drugs for treating conditions

PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or

PT autoimmune diseases.

XX

PS Claim 1; Fig 2; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX

SQ Sequence 16 AA;

Query Match 39.0%; Score 32; DB 6; Length 16;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPFPPK 6
:|||||
Db 8 IKPFPPK 13

RESULT 49

AAE34141

ID AAE34141 standard; peptide; 17 AA.

XX

AC AAE34141;

XX

DT 02-MAY-2003 (first entry)

XX

DE T-cell stimulatory gluten peptide #20.

XX

KW Human leukocyte antigen; HLA; T-cell receptor; giardiasis; celiac sprue;
KW food-related immune enteropathy; tropical sprue; gluten sensitivity;
KW food allergy; protozoacide; antiinflammatory; immunosuppressive; gluten.

XX

OS Unidentified.

XX

PN WO200283722-A2.

XX

PD 24-OCT-2002.

XX
PF 11-APR-2002; 2002WO-NL000235.
XX
PR 12-APR-2001; 2001EP-00201377.
PR 16-NOV-2001; 2001EP-00204383.
XX
PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
XX
PI Drijfhout JW, Koning F, Mcadam SN, Sollid LM;
XX
DR WPI; 2003-093000/08.
XX
PT Novel isolated or recombinant human leukocyte antigen-DQ restricted T-
PT cell receptor for treating food-related immune enteropathy such as celiac
PT sprue, tropical sprue, giardiasis and food allergies of childhood.
XX
PS Disclosure; Fig 2; 64pp; English.
XX
CC The present invention relates to novel isolated or recombinant human
CC leukocyte antigen (HLA)-DQ restricted T-cell receptor or its functional
CC equivalent and/or fragment, capable of recognising a prolamine-derived
CC peptide. The invention relates to recombinant or synthetic prolamine
CC derived peptides involved in food-related immune enteropathy. The
CC pharmaceutical composition is useful to treat food-related immune
CC enteropathies such as celiac sprue, tropical sprue, giardiasis or food
CC allergies of childhood. It is useful to induce tolerance, treat gluten-
CC sensitivity and to eliminate gluten-sensitive T-cells. Sequences of the
CC invention are useful to decrease the amount of toxic prolamine-derived
CC peptides in food or food components and to select and/or breed a cereal.
CC The cereal is useful for inclusion in a diet for a gluten sensitive
CC individual. Blocking substances are useful to decrease the binding of HLA
CC -DQ restricted T-cell receptor to a prolamine-derived peptide involved in
CC food-related immune enteropathy for depletion of T-cells bearing the HLA-
CC DQ restricted T-cell receptor. The present sequence is T-cell stimulatory
CC gluten peptide. This sequence is used in the invention
XX
SQ Sequence 17 AA;

Query Match 39.0%; Score 32; DB 6; Length 17;
Best Local Similarity 46.7%; Pred. No. 1.6e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 4; Gaps 1;

Qy 1 LKPFPPKLKVEVFPFP 15
|:|:|: : |
Db 3 LQPFPPQPQ----PFP 13

RESULT 50

AAR93361

ID AAR93361 standard; peptide; 12 AA.

XX

AC AAR93361;

XX

DT 24-APR-1996 (first entry)

XX

DE LYN protein tyrosine kinase derived peptide #3.

XX

KW SH3 ligand; SH3 binding agent; biased phage library;
 KW recognition sequence; src SH3 domain; Paget's disease; restenosis;
 KW rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47;
 KW p67; complex; chronic myelogenous leukaemia; cancer.
 XX
 OS Synthetic.
 XX
 PN WO9524419-A1.
 XX
 PD 14-SEP-1995.
 XX
 PF 13-MAR-1995; 95WO-US003208.
 XX
 PR 11-MAR-1994; 94US-00209835.
 PR 06-JAN-1995; 95US-00369832.
 XX
 PA (ARIA-) ARIAD PHARM INC.
 XX
 PI Rickles RJ, Brugge JS, Botfield MC, Zoller MJ;
 XX
 DR WPI; 1995-328231/42.
 XX
 PT Identification of peptide(s) binding specifically to SH3 domains - for
 PT use in inhibiting interactions mediated by SH3 domains in treatment of
 PT e.g. osteoporosis and cancer.
 XX
 PS Disclosure; Fig 2; 74pp; English.
 XX
 CC The sequences given in AAR93343-68 represent peptides which are SH3
 CC ligands/SH3 binding agents. They represent a biased phage library which
 CC comprises six random amino acids flanking the hexapeptide RSLRPL- which
 CC was identified as a recognition sequence for the src SH3 domain. These
 CC sequences were identified using the method of the invention. The method
 CC comprises contacting the SH3 domain with a mixture of peptides under
 CC conditions permitting a ligand to bind to an SH3 domain to form a
 CC complex. Any unbound peptides are removed and the complexed peptide
 CC ligands are dissociated from the complexes. The selected peptides are
 CC enriched by re-contacting them with the SH3 domain and then candidates
 CC which bind to the SH3 domain are detected. The isolated SH3 binding
 CC peptides may be used in the diagnosis, prevention and treatment of
 CC conditions or diseases resulting from cellular processes mediated by an
 CC SH3-based interaction. Such diseases include Paget's disease. Other
 CC conditons treatable with these peptides include restenosis, rheumatoid
 CC arthritis, gout and other problems in which an SH3 of neutrophil oxidase
 CC p47 and p67 complex is implicated, etc
 XX
 SQ Sequence 12 AA;

 Query Match 38.4%; Score 31.5; DB 2; Length 12;
 Best Local Similarity 46.7%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 5; Gaps 1;

 Qy 1 LKPFPKLKVEVFPFP 15
 | : | | | | |
 Db 3 LRPLPSL-----PFP 12

Search completed: July 4, 2004, 04:40:56
Job time : 37.1493 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:37:26 ; Search time 9.40299 Seconds
(without alignments)
82.356 Million cell updates/sec

Title: US-09-641-802-8
Perfect score: 82
Sequence: 1 LKPFPKLKVEVFPPF 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121837

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	82	100.0	15	4	US-09-641-803-8	Sequence 8, Appli
2	36	43.9	18	4	US-09-641-803-22	Sequence 22, Appl
3	34	41.5	15	4	US-09-641-803-5	Sequence 5, Appli
4	31	37.8	13	3	US-09-385-442-39	Sequence 39, Appl
5	31	37.8	16	1	US-07-906-871-3	Sequence 3, Appli
6	29	35.4	18	3	US-08-477-928A-26	Sequence 26, Appl
7	28	34.1	14	4	US-09-369-364A-29	Sequence 29, Appl
8	27.5	33.5	14	4	US-08-949-059A-7	Sequence 7, Appli
9	27.5	33.5	14	4	US-08-949-059A-14	Sequence 14, Appl
10	27	32.9	11	1	US-08-347-198A-1	Sequence 1, Appli
11	27	32.9	11	3	US-08-335-844A-25	Sequence 25, Appl

12	27	32.9	11	4	US-09-129-366-25	Sequence 25, Appl
13	27	32.9	14	4	US-09-092-000-1	Sequence 1, Appli
14	27	32.9	16	1	US-08-347-198A-16	Sequence 16, Appl
15	27	32.9	16	3	US-08-335-844A-40	Sequence 40, Appl
16	27	32.9	16	4	US-09-129-366-40	Sequence 40, Appl
17	26.5	32.3	13	3	US-08-915-314-22	Sequence 22, Appl
18	26.5	32.3	13	3	US-08-702-054B-28	Sequence 28, Appl
19	26.5	32.3	13	3	US-08-702-054B-29	Sequence 29, Appl
20	26.5	32.3	13	4	US-09-030-619-93	Sequence 93, Appl
21	26.5	32.3	13	4	US-09-030-619-100	Sequence 100, App
22	26.5	32.3	13	4	US-09-667-486-22	Sequence 22, Appl
23	26	31.7	8	3	US-08-477-928A-46	Sequence 46, Appl
24	26	31.7	8	6	5459077-5	Patent No. 5459077
25	26	31.7	12	1	US-08-347-198A-7	Sequence 7, Appli
26	26	31.7	12	3	US-08-335-844A-31	Sequence 31, Appl
27	26	31.7	12	4	US-09-129-366-31	Sequence 31, Appl
28	26	31.7	13	1	US-08-325-509-34	Sequence 34, Appl
29	26	31.7	15	1	US-08-347-198A-19	Sequence 19, Appl
30	26	31.7	17	4	US-09-552-802B-40	Sequence 40, Appl
31	25	30.5	11	3	US-08-396-385-4	Sequence 4, Appli
32	25	30.5	11	4	US-09-287-221-4	Sequence 4, Appli
33	25	30.5	12	2	US-08-811-492-144	Sequence 144, App
34	25	30.5	12	3	US-08-602-999A-281	Sequence 281, App
35	25	30.5	12	4	US-08-949-059A-30	Sequence 30, Appl
36	25	30.5	12	4	US-09-500-124-281	Sequence 281, App
37	25	30.5	12	4	US-09-446-787B-95	Sequence 95, Appl
38	25	30.5	14	1	US-07-824-247-39	Sequence 39, Appl
39	25	30.5	14	3	US-08-470-204A-39	Sequence 39, Appl
40	25	30.5	15	1	US-08-383-753-43	Sequence 43, Appl
41	25	30.5	15	2	US-08-586-772-43	Sequence 43, Appl
42	25	30.5	15	2	US-08-959-512-43	Sequence 43, Appl
43	25	30.5	15	3	US-09-512-983-43	Sequence 43, Appl
44	25	30.5	16	3	US-08-602-999A-181	Sequence 181, App
45	25	30.5	16	3	US-08-602-999A-239	Sequence 239, App
46	25	30.5	16	4	US-09-029-785-6	Sequence 6, Appli
47	25	30.5	16	4	US-09-500-124-181	Sequence 181, App
48	25	30.5	16	4	US-09-500-124-239	Sequence 239, App
49	25	30.5	16	4	US-09-489-847-252	Sequence 252, App
50	25	30.5	18	3	US-08-974-549A-163	Sequence 163, App
51	25	30.5	18	3	US-09-056-226-7	Sequence 7, Appli
52	25	30.5	18	4	US-09-402-181B-163	Sequence 163, App
53	25	30.5	18	4	US-09-721-456-163	Sequence 163, App
54	24.5	29.9	14	4	US-08-949-059A-25	Sequence 25, Appl
55	24.5	29.9	15	4	US-09-069-827A-100	Sequence 100, App
56	24.5	29.9	15	4	US-09-069-827A-108	Sequence 108, App
57	24	29.3	8	3	US-08-828-712-12	Sequence 12, Appl
58	24	29.3	8	3	US-08-993-165-25	Sequence 25, Appl
59	24	29.3	8	3	US-08-993-165-28	Sequence 28, Appl
60	24	29.3	8	3	US-08-993-165-30	Sequence 30, Appl
61	24	29.3	8	3	US-09-063-276-12	Sequence 12, Appl
62	24	29.3	8	4	US-09-540-448-25	Sequence 25, Appl
63	24	29.3	8	4	US-09-540-448-28	Sequence 28, Appl
64	24	29.3	8	4	US-09-496-761-1	Sequence 1, Appli
65	24	29.3	8	4	US-09-496-761-4	Sequence 4, Appli
66	24	29.3	8	4	US-09-496-761-6	Sequence 6, Appli
67	24	29.3	8	4	US-09-324-782-12	Sequence 12, Appl
68	24	29.3	8	4	US-09-668-143-12	Sequence 12, Appl

69	24	29.3	8	4	US-08-913-612A-46	Sequence 46, Appl
70	24	29.3	8	4	US-08-929-847-26	Sequence 26, Appl
71	24	29.3	8	4	US-08-929-847-29	Sequence 29, Appl
72	24	29.3	9	1	US-08-447-702-2	Sequence 2, Appli
73	24	29.3	9	1	US-08-465-615-2	Sequence 2, Appli
74	24	29.3	9	2	US-08-934-222-128	Sequence 128, App
75	24	29.3	9	2	US-08-933-402-128	Sequence 128, App
76	24	29.3	9	2	US-09-207-621-128	Sequence 128, App
77	24	29.3	9	2	US-08-993-581B-22	Sequence 22, Appl
78	24	29.3	9	2	US-08-532-818-128	Sequence 128, App
79	24	29.3	9	3	US-08-828-712-13	Sequence 13, Appl
80	24	29.3	9	3	US-08-828-712-14	Sequence 14, Appl
81	24	29.3	9	3	US-09-231-797-128	Sequence 128, App
82	24	29.3	9	3	US-08-934-224-128	Sequence 128, App
83	24	29.3	9	3	US-08-933-843-128	Sequence 128, App
84	24	29.3	9	3	US-09-063-276-13	Sequence 13, Appl
85	24	29.3	9	3	US-09-063-276-14	Sequence 14, Appl
86	24	29.3	9	3	US-08-934-223-128	Sequence 128, App
87	24	29.3	9	3	US-09-413-492-128	Sequence 128, App
88	24	29.3	9	4	US-09-324-782-13	Sequence 13, Appl
89	24	29.3	9	4	US-09-324-782-14	Sequence 14, Appl
90	24	29.3	9	4	US-09-668-143-13	Sequence 13, Appl
91	24	29.3	9	4	US-09-668-143-14	Sequence 14, Appl
92	24	29.3	9	4	US-08-913-612A-47	Sequence 47, Appl
93	24	29.3	12	4	US-09-419-826-30	Sequence 30, Appl
94	24	29.3	12	6	5284931-36	Patent No. 5284931
95	24	29.3	13	1	US-08-477-509B-20	Sequence 20, Appl
96	24	29.3	13	4	US-09-444-791A-20	Sequence 20, Appl
97	24	29.3	13	4	US-09-486-283C-83	Sequence 83, Appl
98	24	29.3	13	4	US-09-486-283C-178	Sequence 178, App
99	24	29.3	14	4	US-09-758-008-13	Sequence 13, Appl
100	24	29.3	15	2	US-08-480-190-238	Sequence 238, App

ALIGNMENTS

RESULT 1
 US-09-641-803-8
 ; Sequence 8, Application US/09641803
 ; Patent No. 6500798
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
 ; FILE REFERENCE: 265.00220101
 ; CURRENT APPLICATION NUMBER: US/09/641,803
 ; CURRENT FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 15
 ; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-8

Query Match 100.0%; Score 82; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVFPFP 15
| | | | | | | | | | | | | | |
Db 1 LKPFPKLKVEVFPFP 15

RESULT 2

US-09-641-803-22
; Sequence 22, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-22

Query Match 43.9%; Score 36; DB 4; Length 18;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PFPKLVKVEVF 12
| | | | | | |
Db 5 PFPKYPVEPF 14

RESULT 3

US-09-641-803-5
; Sequence 5, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.

```

; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-5

```

```

Query Match          41.5%; Score 34; DB 4; Length 15;
Best Local Similarity 70.0%; Pred. No. 23;
Matches      7; Conservative    0; Mismatches    3; Indels      0; Gaps      0;

```

```

Qy      5 PKLKVEVFPPF 14
        | | || |||
Db      5 PVLPEVFPPF 14

```

RESULT 4

```

US-09-385-442-39
; Sequence 39, Application US/09385442
; Patent No. 6200954
; GENERAL INFORMATION:
; APPLICANT: Ge, Ruowen
; APPLICANT: Kini, R. Manjunatha
; TITLE OF INVENTION: Small Peptides Having Potent Anti-Angiogenic Activity
; FILE REFERENCE: 1781-170P
; CURRENT APPLICATION NUMBER: US/09/385,442
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 60/099,313
; EARLIER FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 13
; TYPE: PRT
; ORGANISM: mammalian
; FEATURE:
; OTHER INFORMATION: shFLT2
US-09-385-442-39

```

```

Query Match          37.8%; Score 31; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 60;
Matches      6; Conservative    1; Mismatches    5; Indels      0; Gaps      0;

```

```

Qy      1 LKPFPKLKVEVF 12
        | | ||:| |

```

RESULT 5

US-07-906-871-3

; Sequence 3, Application US/07906871

; Patent No. 5340739

; GENERAL INFORMATION:

; APPLICANT: Stevens, Richard L.

; APPLICANT: Avraham, Shalom

; TITLE OF INVENTION: HEMATOPOIETIC CELL SPECIFIC

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY ELEMENTS OF SERGLYCIN AND
USES

; TITLE OF INVENTION: THEREOF

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1225 Connecticut Avenue, N.W., Suite 300

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/906,871

; FILING DATE: 19920103

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/816,289

; FILING DATE: 03 JAN 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/635,544

; FILING DATE: 18-JAN-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US89/03051

; FILING DATE: 13-JUL-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/224,035

; FILING DATE: 13-JUL-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Cimbala, Michele A

; REGISTRATION NUMBER: 33,851

; REFERENCE/DOCKET NUMBER: 0627.2830004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)833-7533

; TELEFAX: (202)833-8716

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: both

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-07-906-871-3

Query Match 37.8%; Score 31; DB 1; Length 16;
Best Local Similarity 44.4%; Pred. No. 74;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PKLKVEVFP 13
|:|: ::||
Db 5 PRLRTDLFP 13

RESULT 6

US-08-477-928A-26

; Sequence 26, Application US/08477928A
; Patent No. 6207389
; GENERAL INFORMATION:
; APPLICANT: Dosch, Hans M.
; TITLE OF INVENTION: METHODS FOR CONTROLLING T
; TITLE OF INVENTION: LYMPHOCYTE MEDIATED IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS
; STREET: 1299 Pennsylvania Avenue
; CITY: Washington D.C.
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,928A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36902
; REFERENCE/DOCKET NUMBER: 19060-0105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 639 7700
; TELEFAX: (202) 639 7890
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-477-928A-26

Query Match 35.4%; Score 29; DB 3; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KPFPKLKVEV 11

Db | | |||::|
 4 KNFDKCLKMDV 13

RESULT 7

US-09-369-364A-29
; Sequence 29, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-369-364A-29

Query Match 34.1%; Score 28; DB 4; Length 14;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKPFPKLK 8
 :| | | |:
Db 6 IKPKPKLQ 13

RESULT 8

US-08-949-059A-7
; Sequence 7, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk


```

;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/949,059A
;      FILING DATE:  10-OCT-1997
;      CLASSIFICATION:  514
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  660081.412
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;      INFORMATION FOR SEQ ID NO:  7:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  cyclic
;      MOLECULE TYPE:  peptide
;      HYPOTHETICAL:  NO
;      ANTI-SENSE:  NO
;      FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  13
;      OTHER INFORMATION:  /note= "Residue is a D-Tyrosine"
US-08-949-059A-7

```

```

Query Match          33.5%;  Score 27.5;  DB 4;  Length 14;
Best Local Similarity  53.8%;  Pred. No. 2.4e+02;
Matches      7;  Conservative      3;  Mismatches      2;  Indels      1;  Gaps      1;

```

```

Qy      1 LKPFPKLKVEVFP 13
        || :| |||:: |
Db      3 LKVYP-LKVKLXP 14

```

RESULT 9

US-08-949-059A-14

```

; Sequence 14, Application US/08949059A
; Patent No. 6358921

```

; GENERAL INFORMATION:

```

;  APPLICANT:  Kondejewski, Leslie H.
;  APPLICANT:  Hodges, Robert S.
;  APPLICANT:  Wishart, David S.
;  APPLICANT:  Hancock, Robert E.W.
;  APPLICANT:  McElhaney, Ronald N.
;  APPLICANT:  Prenner, Elmar J.
;  APPLICANT:  Lewis, Ruthven N.A.H
;  TITLE OF INVENTION:  ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
;  TITLE OF INVENTION:  METHOD
;  NUMBER OF SEQUENCES:  42
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE:  SEED and BERRY LLP
;  STREET:  6300 Columbia Center, 701 Fifth Avenue
;  CITY:  Seattle

```

```

; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
US-08-949-059A-14

```

```

Query Match          33.5%; Score 27.5; DB 4; Length 14;
Best Local Similarity 53.8%; Pred. No. 2.4e+02;
Matches      7; Conservative      3; Mismatches      2; Indels      1; Gaps      1;

```

```

Qy      1 LKPFPLKVEVFP 13
        || | |||:::|
Db      3 LKVXP-LKVKLYP 14

```

RESULT 10

US-08-347-198A-1

```

; Sequence 1, Application US/08347198A
; Patent No. 5747046

```

GENERAL INFORMATION:

```

; APPLICANT: MUNN, Edward A.
; APPLICANT: SMITH, Trevor S.
; TITLE OF INVENTION: PRODUCTION AND USE OF ANTHELMINTIC
; TITLE OF INVENTION: AGENTS AND PROTECTIVE IMMUNOGENS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; STREET: Street Lobby

```

```

; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,198A
; FILING DATE: 21-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/020,526
; FILING DATE: 22-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/761,749
; FILING DATE: 17-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB90/00416
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 89906156.8
; FILING DATE: 17-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P443-1289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-347-198A-1

```

```

Query Match          32.9%; Score 27; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches      5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      4 FPKLKVEVF 12
        :| :||| |
Db      3 YPVVKVEEF 11

```

```

RESULT 11
US-08-335-844A-25
; Sequence 25, Application US/08335844A
; Patent No. 6066503
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY

```

```

;   APPLICANT:  MUNN, EDWARD ALBERT
;   APPLICANT:  KNOX, DAVID PATRICK
;   APPLICANT:  OLIVER, JOANNA JANE
;   APPLICANT:  NEWTON, SUSAN ELIZABETH
;   TITLE OF INVENTION:  RECOMBINANT DNA MOLECULES ENCODING
;   TITLE OF INVENTION:  AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE
PREPARATION OF
;   TITLE OF INVENTION:  VACCINES AGAINST HELMINTH INFECTIONS
;   NUMBER OF SEQUENCES:  73
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Rothwell, Figg, Ernst & Kurz
;     STREET:    Suite 701-E, 555 Thirteenth St., N.W
;     CITY:      Washington
;     STATE:     D. C.
;     COUNTRY:   U.S.A.
;     ZIP:       20004
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/335,844A
;     FILING DATE:       09-JAN-1995
;     CLASSIFICATION:    424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  GB PCT/GB93/00943
;     FILING DATE:        06-MAY-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  GB 9209936
;     FILING DATE:        08-MAY-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME:               WALKER, Barbara W.
;     REGISTRATION NUMBER: 35,400
;     REFERENCE/DOCKET NUMBER: 1181-223A
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:          (202)783-6040
;     TELEFAX:            (202)783-6031
;   INFORMATION FOR SEQ ID NO: 25:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       STRANDEDNESS:
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-08-335-844A-25

```

```

Query Match          32.9%;  Score 27;  DB 3;  Length 11;
Best Local Similarity 55.6%;  Pred. No. 2.2e+02;
Matches      5;  Conservative      2;  Mismatches      2;  Indels      0;  Gaps      0;

```

```

Qy      4 FPKLKVEVF 12
        :| :||| |
Db      3 YPVVKVEEF 11

```

RESULT 12

US-09-129-366-25
 ; Sequence 25, Application US/09129366
 ; Patent No. 6534638
 ; GENERAL INFORMATION:
 ; APPLICANT: GRAHAM, MARGARET
 ; APPLICANT: SMITH, TREVOR STANLEY
 ; APPLICANT: MUNN, EDWARD ALBERT
 ; APPLICANT: KNOX, DAVID PATRICK
 ; APPLICANT: OLIVER, JOANNA JANE
 ; APPLICANT: NEWTON, SUSAN ELIZABETH
 ; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
 ; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE
 PREPARATION OF
 ; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
 ; NUMBER OF SEQUENCES: 73
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
 ; STREET: Suite 701-E, 555 Thirteenth St., N.W
 ; CITY: Washington
 ; STATE: D. C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/129,366
 ; FILING DATE: 05-AUG-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/335,844
 ; FILING DATE: 09-JAN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB PCT/GB93/00943
 ; FILING DATE: 06-MAY-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9209936
 ; FILING DATE: 08-MAY-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: ERNST, Barbara G.
 ; REGISTRATION NUMBER: 30,377
 ; REFERENCE/DOCKET NUMBER: 1181-241A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)783-6040
 ; TELEFAX: (202)783-6031
 ; INFORMATION FOR SEQ ID NO: 25:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-09-129-366-25

Query Match

32.9%; Score 27; DB 4; Length 11;

Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FPKLKVEVF 12
:| :||| |
Db 3 YPVVKVEEF 11

RESULT 13

US-09-092-000-1

; Sequence 1, Application US/09092000
; Patent No. 6339139
; GENERAL INFORMATION:
; APPLICANT: Gu, Jian-ren
; APPLICANT: Tian, Peikun
; TITLE OF INVENTION: Receptor-Mediated Gene Transfer SYstem for Targeting
; TITLE OF INVENTION: Tumor Gene Therapy
; FILE REFERENCE: Gu
; CURRENT APPLICATION NUMBER: US/09/092,000
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 96 116557.X
; EARLIER FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: PCT/CN97/00106
; EARLIER FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ligand
; OTHER INFORMATION: oligopeptide for the receptor region of IGF I and
; OTHER INFORMATION: IGF II
US-09-092-000-1

Query Match 32.9%; Score 27; DB 4; Length 14;
Best Local Similarity 46.2%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

Qy 2 KPF--PKLKVEVF 12
:|| ||| :| :
Db 1 EPFRSPKLALETY 13

RESULT 14

US-08-347-198A-16

; Sequence 16, Application US/08347198A
; Patent No. 5747046
; GENERAL INFORMATION:
; APPLICANT: MUNN, Edward A.
; APPLICANT: SMITH, Trevor S.
; TITLE OF INVENTION: PRODUCTION AND USE OF ANTHELMINTIC
; TITLE OF INVENTION: AGENTS AND PROTECTIVE IMMUNOGENS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP

```

; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; STREET: Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,198A
; FILING DATE: 21-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/020,526
; FILING DATE: 22-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/761,749
; FILING DATE: 17-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB90/00416
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 89906156.8
; FILING DATE: 17-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P443-1289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-347-198A-16

```

```

Query Match          32.9%; Score 27; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 3.3e+02;
Matches      5; Conservative      2; Mismatches      2; Indels      0; Gaps      0;

```

```

Qy      4 FPKLKVEVF 12
        :| :||| |
Db      3 YPVVKVEEF 11

```

```

RESULT 15
US-08-335-844A-40
; Sequence 40, Application US/08335844A
; Patent No. 6066503
; GENERAL INFORMATION:

```

```

; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE
PREPARATION OF
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,844A
; FILING DATE: 09-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 1181-223A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-335-844A-40

```

```

Query Match          32.9%; Score 27; DB 3; Length 16;
Best Local Similarity 55.6%; Pred. No. 3.3e+02;
Matches      5; Conservative      2; Mismatches      2; Indels      0; Gaps      0;

```

```

Qy      4 FPKLKVEVF 12
        :| :||| |
Db      3 YPVVKVEEF 11

```


RESULT 16

US-09-129-366-40

; Sequence 40, Application US/09129366

; Patent No. 6534638

; GENERAL INFORMATION:

; APPLICANT: GRAHAM, MARGARET

; APPLICANT: SMITH, TREVOR STANLEY

; APPLICANT: MUNN, EDWARD ALBERT

; APPLICANT: KNOX, DAVID PATRICK

; APPLICANT: OLIVER, JOANNA JANE

; APPLICANT: NEWTON, SUSAN ELIZABETH

; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING

; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE
PREPARATION OF

; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rothwell, Figg, Ernst & Kurz

; STREET: Suite 701-E, 555 Thirteenth St., N.W

; CITY: Washington

; STATE: D. C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/129,366

; FILING DATE: 05-AUG-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/335,844

; FILING DATE: 09-JAN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB PCT/GB93/00943

; FILING DATE: 06-MAY-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9209936

; FILING DATE: 08-MAY-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: ERNST, Barbara G.

; REGISTRATION NUMBER: 30,377

; REFERENCE/DOCKET NUMBER: 1181-241A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)783-6040

; TELEFAX: (202)783-6031

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-129-366-40

Query Match 32.9%; Score 27; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 3.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FPKLKVEVF 12
:|:| | |
Db 3 YPVVKVEEF 11

RESULT 17

US-08-915-314-22

; Sequence 22, Application US/08915314
; Patent No. 6180604

; GENERAL INFORMATION:

; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfle, Douglas
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/915,314
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 6180604tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 660081.405

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

US-08-915-314-22

Query Match 32.3%; Score 26.5; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 LKPFPKLVKVEVFPF 14
 || || |||
 Db 2 LKKFP-----FFPF 10

RESULT 18

US-08-702-054B-28

; Sequence 28, Application US/08702054B
 ; Patent No. 6191254
 ; GENERAL INFORMATION:
 ; APPLICANT: Falls, Timothy J.
 ; APPLICANT: Hancock, Robert E. W.
 ; APPLICANT: Gough, Monisha
 ; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
 ; TITLE OF INVENTION: AND METHODS OF SCREENING FOR THE SAME
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/702,054B
 ; FILING DATE: 23-AUG-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/002,687
 ; FILING DATE: 23-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haile, Lisa A.
 ; REGISTRATION NUMBER: 38,347
 ; REFERENCE/DOCKET NUMBER: 07420/013001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619/678-5070
 ; TELEFAX: 619/678-5099
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-702-054B-28

Query Match 32.3%; Score 26.5; DB 3; Length 13;
 Best Local Similarity 50.0%; Pred. No. 3.2e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 LKPFPKLVKVEVFPF 14
 || || |||
 Db 2 LKKFP-----FFPF 10

RESULT 19

US-08-702-054B-29

; Sequence 29, Application US/08702054B
 ; Patent No. 6191254
 ; GENERAL INFORMATION:
 ; APPLICANT: Falls, Timothy J.
 ; APPLICANT: Hancock, Robert E. W.
 ; APPLICANT: Gough, Monisha
 ; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
 ; TITLE OF INVENTION: AND METHODS OF SCREENING FOR THE SAME
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/702,054B
 ; FILING DATE: 23-AUG-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/002,687
 ; FILING DATE: 23-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haile, Lisa A.
 ; REGISTRATION NUMBER: 38,347
 ; REFERENCE/DOCKET NUMBER: 07420/013001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619/678-5070
 ; TELEFAX: 619/678-5099
 ; INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

US-08-702-054B-29

Query Match 32.3%; Score 26.5; DB 3; Length 13;
 Best Local Similarity 50.0%; Pred. No. 3.2e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 LKPFPPKLKVEVFPF 14
 || || ||
 Db 2 LKKFP-----FFPF 10

RESULT 20

US-09-030-619-93

```

; Sequence 93, Application US/09030619B
; Patent No. 6503881
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfle, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN
COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 93
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-93

```

```

Query Match          32.3%; Score 26.5; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches      7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

```

```

Qy      1 LKPFPKLKVEVFPF 14
        || ||      |||
Db      2 LKKFP-----FFPF 10

```

RESULT 21

```

US-09-030-619-100
; Sequence 100, Application US/09030619B
; Patent No. 6503881
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfle, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN
COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 13

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-100

Query Match 32.3%; Score 26.5; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 LKPFPLKVEVFPF 14
|| || ||
Db 2 LKKFP-----FFPF 10

RESULT 22

US-09-667-486-22

; Sequence 22, Application US/09667486
; Patent No. 6538106

; GENERAL INFORMATION:

; APPLICANT: Fraser, Janet R.
; West, Michael H.P.
; Krieger, Timothy J.
; Taylor, Robert
; Erfle, Douglas

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; INFECTIONS USING ANALOGUES OF INDOLICIDIN

; NUMBER OF SEQUENCES: 90

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/667,486
; FILING DATE: 22-Sep-2000
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/915,314
; FILING DATE: 20-AUG-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 6538106tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 660081.405

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids

; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-667-486-22

Query Match 32.3%; Score 26.5; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 LKPFPKLKVEVFPP 14
|| || ||
Db 2 LKKFP-----FFPF 10

RESULT 23

US-08-477-928A-46

; Sequence 46, Application US/08477928A
; Patent No. 6207389
; GENERAL INFORMATION:
; APPLICANT: Dosch, Hans M.
; TITLE OF INVENTION: METHODS FOR CONTROLLING T
; TITLE OF INVENTION: LYMPHOCYTE MEDIATED IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS
; STREET: 1299 Pennsylvania Avenue
; CITY: Washington D.C.
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,928A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36902
; REFERENCE/DOCKET NUMBER: 19060-0105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 639 7700
; TELEFAX: (202) 639 7890
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-928A-46

Query Match 31.7%; Score 26; DB 3; Length 8;

Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FPKLKVEV 11
| |||::|
Db 1 FDKLKMDV 8

RESULT 24

5459077-5

; Patent No. 5459077

; APPLICANT: MOORE, GRAHAM J.; MATSOUKAS, JOHN M.

; TITLE OF INVENTION: METHODS FOR MODELLING TERTIARY STRUCTURES

; OF BIOLOGICALLY ACTIVE LIGANDS AND FOR MODELLING AGONISTS AND

; ANTIGONISTS THERETO

; NUMBER OF SEQUENCES: 9

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/27,561

; FILING DATE: 05-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 458,926

; FILING DATE: 29-DEC-1989

; SEQ ID NO: 5:

; LENGTH: 8

5459077-5

Query Match 31.7%; Score 26; DB 6; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KVEVFPPF 14
:| :|||
Db 2 RVIIFPPF 8

RESULT 25

US-08-347-198A-7

; Sequence 7, Application US/08347198A

; Patent No. 5747046

; GENERAL INFORMATION:

; APPLICANT: MUNN, Edward A.

; APPLICANT: SMITH, Trevor S.

; TITLE OF INVENTION: PRODUCTION AND USE OF ANTHELMINTIC

; TITLE OF INVENTION: AGENTS AND PROTECTIVE IMMUNOGENS

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIKAIDO, MARMELESTEIN, MURRAY & ORAM LLP

; STREET: 655 Fifteenth Street, N. W., Suite 330 - G

; STREET: Street Lobby

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-5701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS


```

;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/347,198A
;   FILING DATE: 21-NOV-1994
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/020,526
;   FILING DATE: 22-FEB-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/761,749
;   FILING DATE: 17-SEP-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/GB90/00416
;   FILING DATE: 19-MAR-1990
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: GB 89906156.8
;   FILING DATE: 17-MAR-1989
;   ATTORNEY/AGENT INFORMATION:
;   NAME: KITTS, Monica C.
;   REGISTRATION NUMBER: 36,105
;   REFERENCE/DOCKET NUMBER: P443-1289
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202/638-5000
;   TELEFAX: 202/638-4810
;   INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 12 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-347-198A-7

```

```

Query Match          31.7%; Score 26; DB 1; Length 12;
Best Local Similarity 55.6%; Pred. No. 3.5e+02;
Matches      5; Conservative      1; Mismatches      3; Indels      0; Gaps      0;

```

```

Qy      4 FPKLKVEVF 12
        || : || |
Db      3 FPLVTVEAF 11

```

RESULT 26

US-08-335-844A-31

```

; Sequence 31, Application US/08335844A
; Patent No. 6066503
; GENERAL INFORMATION:
;   APPLICANT: GRAHAM, MARGARET
;   APPLICANT: SMITH, TREVOR STANLEY
;   APPLICANT: MUNN, EDWARD ALBERT
;   APPLICANT: KNOX, DAVID PATRICK
;   APPLICANT: OLIVER, JOANNA JANE
;   APPLICANT: NEWTON, SUSAN ELIZABETH
;   TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
;   TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE
PREPARATION OF
;   TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS

```

```

; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,844A
; FILING DATE: 09-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 1181-223A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-335-844A-31

```

```

Query Match          31.7%; Score 26; DB 3; Length 12;
Best Local Similarity 55.6%; Pred. No. 3.5e+02;
Matches      5; Conservative      1; Mismatches      3; Indels      0; Gaps      0;

```

```

Qy      4 FPKLKVEVF 12
        || : || |
Db      3 FPLVTVEAF 11

```

RESULT 27

US-09-129-366-31

```

; Sequence 31, Application US/09129366
; Patent No. 6534638
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK

```

```

; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE
PREPARATION OF
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/129,366
; FILING DATE: 05-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,844
; FILING DATE: 09-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1181-241A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-129-366-31

```

```

Query Match          31.7%; Score 26; DB 4; Length 12;
Best Local Similarity 55.6%; Pred. No. 3.5e+02;
Matches      5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      4 FPKLKVEVF 12
        || : || |
Db      3 FPLVTVEAF 11

```

RESULT 28

US-08-325-509-34

```
; Sequence 34, Application US/08325509
; Patent No. 5543308
; GENERAL INFORMATION:
;   APPLICANT: MORGAN, RICHARD D.
;   TITLE OF INVENTION: ISOLATED DNA ENCODING THE FseI
;   TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND RELATED METHODS FOR
;   TITLE OF INVENTION: PRODUCING THE SAME
;   NUMBER OF SEQUENCES: 55
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND
;     ADDRESSEE: BIOLABS, INC.
;     STREET: 32 TOZER ROAD
;     CITY: BEVERLY
;     STATE: MASSACHUSETTS
;     COUNTRY: US
;     ZIP: 01915
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/325,509
;     FILING DATE: 18-OCT-1994
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: WILLIAMS, GREGORY D.
;     REGISTRATION NUMBER: 30901
;     REFERENCE/DOCKET NUMBER: NEB-104
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (508) 927-5054
;     TELEFAX: (508) 927-1705
;   INFORMATION FOR SEQ ID NO: 34:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 13 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: unknown
;       TOPOLOGY: unknown
;     MOLECULE TYPE: protein
```

US-08-325-509-34

```
Query Match          31.7%;  Score 26;  DB 1;  Length 13;
Best Local Similarity 66.7%;  Pred. No. 3.8e+02;
Matches      4;  Conservative    1;  Mismatches    1;  Indels      0;  Gaps      0;
```

```
Qy      10 EVFPFP 15
          |:|| |
Db      4  ELFPIP 9
```

RESULT 29

US-08-347-198A-19

```
; Sequence 19, Application US/08347198A
; Patent No. 5747046
; GENERAL INFORMATION:
```

```

; APPLICANT: MUNN, Edward A.
; APPLICANT: SMITH, Trevor S.
; TITLE OF INVENTION: PRODUCTION AND USE OF ANTHELMINTIC
; TITLE OF INVENTION: AGENTS AND PROTECTIVE IMMUNOGENS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; STREET: Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,198A
; FILING DATE: 21-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/020,526
; FILING DATE: 22-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/761,749
; FILING DATE: 17-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB90/00416
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 89906156.8
; FILING DATE: 17-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P443-1289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-347-198A-19

```

```

Query Match          31.7%; Score 26; DB 1; Length 15;
Best Local Similarity 55.6%; Pred. No. 4.4e+02;
Matches      5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      4 FPKLKVEVF 12
        || : || |
Db      3 FPLVTVEAF 11

```

RESULT 30

US-09-552-802B-40

```
; Sequence 40, Application US/09552802B
; Patent No. 6562943
; GENERAL INFORMATION:
; APPLICANT: Peakman, Mark
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: PEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
; TITLE OF INVENTION: CD4+ T LYMPHOCYTES
; FILE REFERENCE: 08191-009002
; CURRENT APPLICATION NUMBER: US/09/552,802B
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/295,868
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/130,355
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-552-802B-40
```

```
Query Match          31.7%; Score 26; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches      6; Conservative      0; Mismatches      2; Indels      0; Gaps      0;
```

```
Qy          6 KLKVEVFP 13
             ||||| |
Db          1 KLKVESSP 8
```

RESULT 31

US-08-396-385-4

```
; Sequence 4, Application US/08396385
; Patent No. 6001349
; GENERAL INFORMATION:
; APPLICANT: Schlom, Jeffrey
; APPLICANT: Panicali, Dennis
; TITLE OF INVENTION: GENERATION OF HUMAN CYTOTOXIC T-CELLS
; TITLE OF INVENTION: SPECIFIC FOR CARCINOMA SELF-ASSOCIATED ANTIGENS AND
USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEWALL P. BRONSTEIN; DIKE, BRONSTEIN, ROBERTS
; ADDRESSEE: & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```

;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/396,385
;      FILING DATE:
;      CLASSIFICATION:  530
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Resnick, David S.
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  44933
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 523-3400
;      TELEFAX:  (617) 523-6440
;      TELEX:  200291 STRE UR
;      INFORMATION FOR SEQ ID NO:  4:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
US-08-396-385-4

```

```

Query Match          30.5%;  Score 25;  DB 3;  Length 11;
Best Local Similarity  55.6%;  Pred. No. 4.6e+02;
Matches      5;  Conservative  1;  Mismatches  3;  Indels    0;  Gaps    0;

```

```

Qy      6 KLKVEVFPF 14
        || :|  ||
Db      1 KLTIIESTPF 9

```

RESULT 32

US-09-287-221-4

```

; Sequence 4, Application US/09287221
; Patent No. 6319496

```

GENERAL INFORMATION:

```

; APPLICANT:  Schlom, Jeffrey
; APPLICANT:  Panicali, Dennis
; TITLE OF INVENTION:  GENERATION OF HUMAN CYTOTOXIC T-CELLS
; TITLE OF INVENTION:  SPECIFIC FOR CARCINOMA SELF-ASSOCIATED ANTIGENS AND
USES

```

```

; TITLE OF INVENTION:  THEREOF
; NUMBER OF SEQUENCES:  12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  SEWALL P. BRONSTEIN; DIKE, BRONSTEIN, ROBERTS
; ADDRESSEE:  & CUSHMAN
; STREET:  130 WATER STREET
; CITY:  BOSTON
; STATE:  MASSACHUSETTS
; COUNTRY:  US
; ZIP:  02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.25

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/287,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/396,385
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44933
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-09-287-221-4

```

```

Query Match          30.5%; Score 25; DB 4; Length 11;
Best Local Similarity 55.6%; Pred. No. 4.6e+02;
Matches      5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      6 KLKVEVFPF 14
        || :|  ||
Db      1 KLTIESTPF 9

```

```

RESULT 33
US-08-811-492-144
; Sequence 144, Application US/08811492
; Patent No. 5834247
; GENERAL INFORMATION:
; APPLICANT: COMB, DONALD G.
; APPLICANT: PERLER, FRANCINE B.
; APPLICANT: JACK, WILLIAM E.
; APPLICANT: XU, MING-QUN
; APPLICANT: HODGES, ROBERT A.
; APPLICANT: NOREN, CHRISTOPHER J.
; APPLICANT: CHONG, SHAORONG S.C.
; APPLICANT: ADAM, ERIC
; APPLICANT: SOUTHWORTH, MAURICE
; TITLE OF INVENTION: MODIFIED PROTEINS, METHODS OF THEIR
; TITLE OF INVENTION: PRODUCTION AND METHODS FOR PURIFICATION OF TARGET
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 155
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER RAOD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915

```



```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC\_DOS/MS\_DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,492
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/580,555
; FILING DATE: 29-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,247
; FILING DATE: 28-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,885
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/004,139
; FILING DATE: 09-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-036C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-927-5054
; TELEFAX: 509-927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 144:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-811-492-144

```

```

Query Match          30.5%; Score 25; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 5.1e+02;
Matches      4; Conservative      4; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      1 LKPFPKLV 9
        |: :|::||
Db      3 LQHYPRVKV 11

```

```

RESULT 34
US-08-602-999A-281
; Sequence 281, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.

```

```

; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 281:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-281

```

```

Query Match          30.5%; Score 25; DB 3; Length 12;
Best Local Similarity 50.0%; Pred. No. 5.1e+02;
Matches      4; Conservative      2; Mismatches      2; Indels      0; Gaps      0;

```

```

Qy      2 KPFPKLV 9
        :| ||: |
Db      4 RPIPKVPV 11

```

```

RESULT 35
US-08-949-059A-30
; Sequence 30, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.

```

```

; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
US-08-949-059A-30

```

```

Query Match          30.5%; Score 25; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 PKLKV 9
        |||||
Db      8 PKLKV 12

```

RESULT 36

US-09-500-124-281

; Sequence 281, Application US/09500124

; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/500,124

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/602,999

; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 281:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-09-500-124-281

Query Match 30.5%; Score 25; DB 4; Length 12;

Best Local Similarity 50.0%; Pred. No. 5.1e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy

2 KPFPKLV 9

Db :| ||: |
 4 RPIPKVPV 11

RESULT 37

US-09-446-787B-95
; Sequence 95, Application US/09446787B
; Patent No. 6541198
; GENERAL INFORMATION:
; APPLICANT: Akzo No. 6541198el N.V.
; APPLICANT: Paulij, Wilhemina P.
; APPLICANT: Van Kessel-Koens, Marjolijn J.
; TITLE OF INVENTION: Antibodies and other binding molecules specific for
hepatitis B viral
; TITLE OF INVENTION: antigens
; FILE REFERENCE: 9310-19
; CURRENT APPLICATION NUMBER: US/09/446,787B
; CURRENT FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-446-787B-95

Query Match 30.5%; Score 25; DB 4; Length 12;
Best Local Similarity 44.4%; Pred. No. 5.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PKLKVEVFP 13
 |:::| ||
Db 3 PRVRVLYFP 11

RESULT 38

US-07-824-247-39
; Sequence 39, Application US/07824247
; Patent No. 5512482
; GENERAL INFORMATION:
; APPLICANT: Voelker, Toni Alois
; TITLE OF INVENTION: Plant Thioesterases
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: MicrosoftWord 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/824,247

```

; FILING DATE: 19920122
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/782,263
; FILING DATE: 24-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/773,096
; FILING DATE: 7-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/704,861
; FILING DATE: 21-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02960
; FILING DATE: 25-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,007
; FILING DATE: 27-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/620,426
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/514,030
; FILING DATE: 26-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 82-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 916-753-6313
; TELEFAX: 916-753-1510
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-824-247-39

```

```

Query Match          30.5%; Score 25; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches      5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 KPFPKL 7
        || |||
Db      4 KPFPKL 9

```

```

RESULT 39
US-08-470-204A-39
; Sequence 39, Application US/08470204A
; Patent No. 6028247
; GENERAL INFORMATION:
; APPLICANT: Voelker, Toni Alois
; TITLE OF INVENTION: Plant Thioesterases
; NUMBER OF SEQUENCES: 48

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
; COMPUTER: Apple Macintosh IIci
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: MicrosoftWord 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,204A
; FILING DATE: 06-JUN-95
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/824,247
; FILING DATE: 22-JAN-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/782,263
; FILING DATE: 24-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/773,096
; FILING DATE: 7-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/704,861
; FILING DATE: 21-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02960
; FILING DATE: 25-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,007
; FILING DATE: 27-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/620,426
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/514,030
; FILING DATE: 26-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 82-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 916-753-6313
; TELEFAX: 916-753-1510
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-470-204A-39

Query Match 30.5%; Score 25; DB 3; Length 14;
Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPFPKL 7
|| |||
Db 4 KPKPKL 9

RESULT 40

US-08-383-753-43

; Sequence 43, Application US/08383753
; Patent No. 5723584
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; TITLE OF INVENTION: Biotinylation of Proteins
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,753
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/099,991
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 1038.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-753-43

Query Match 30.5%; Score 25; DB 1; Length 15;
Best Local Similarity 38.5%; Pred. No. 6.4e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVFP 13
|:| :|:| |
Db 2 LQTFDAMKMEWLP 14

RESULT 41

US-08-586-772-43

; Sequence 43, Application US/08586772

; Patent No. 5874239

; GENERAL INFORMATION:

; APPLICANT: Schatz, Peter J.

; TITLE OF INVENTION: Biotinylation of Proteins

; NUMBER OF SEQUENCES: 102

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: One Market Plaza, Steuart Tower

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/586,772

; FILING DATE: 03-FEB-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/099,991

; FILING DATE: 30-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 1038.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-586-772-43

Query Match 30.5%; Score 25; DB 2; Length 15;

Best Local Similarity 38.5%; Pred. No. 6.4e+02;

Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVFP 13
|:| :|:| |
Db 2 LQTFDAMKMEWLP 14

RESULT 42

US-08-959-512-43

```
; Sequence 43, Application US/08959512
; Patent No. 5932433
; GENERAL INFORMATION:
;   APPLICANT:  Schatz, Peter J.
;   TITLE OF INVENTION:  Biotinylation of Proteins
;   NUMBER OF SEQUENCES:  102
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Townsend and Townsend Khourie and Crew
;     STREET:  One Market Plaza, Steuart Tower
;     CITY:  San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94105
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/959,512
;     FILING DATE:
;     CLASSIFICATION:  530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/383,753
;     FILING DATE:  03-FEB-1995
;     APPLICATION NUMBER:  US 08/099,991
;     FILING DATE:  30-JUL-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Smith, William M.
;     REGISTRATION NUMBER:  30,223
;     REFERENCE/DOCKET NUMBER:  1038.1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415-326-2400
;     TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  43:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
```

US-08-959-512-43

```
Query Match          30.5%;  Score 25;  DB 2;  Length 15;
Best Local Similarity 38.5%;  Pred. No. 6.4e+02;
Matches      5;  Conservative  3;  Mismatches  5;  Indels  0;  Gaps  0;
```

```
Qy      1 LKPFPKLKVEVFP 13
          |:|  :|:|  |
Db      2 LQTFDAMKMEWLP 14
```

RESULT 43

US-09-512-983-43

```
; Sequence 43, Application US/09512983
```

```

; Patent No. 6265552
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; TITLE OF INVENTION: Biotinylation of Proteins
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/512,983
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,753
; FILING DATE: 03-FEB-1995
; APPLICATION NUMBER: US 08/099,991
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 1038.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-512-983-43

```

```

Query Match          30.5%; Score 25; DB 3; Length 15;
Best Local Similarity 38.5%; Pred. No. 6.4e+02;
Matches      5; Conservative      3; Mismatches      5; Indels      0; Gaps      0;

```

```

Qy      1 LKPFPKPKVEVFP 13
        |:| :|:| |
Db      2 LQTFDAMKMEWLP 14

```

```

RESULT 44
US-08-602-999A-181
; Sequence 181, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.

```

```

; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-181

```

```

Query Match          30.5%; Score 25; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches      4; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      3 PFPK 6
      ||||
Db      5 PFPK 8

```

RESULT 45

```

US-08-602-999A-239
; Sequence 239, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.

```

```

; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 239:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-239

```

```

Query Match          30.5%; Score 25; DB 3; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.8e+02;
Matches      5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy      1 LKPFPKLKVEV 11
        | | |: | |
Db      6 LPPIPQSKTSV 16

```

```

RESULT 46
US-09-029-785-6
; Sequence 6, Application US/09029785B
; Patent No. 6388175
; GENERAL INFORMATION:
; APPLICANT: BIRCH, ROBERT
; APPLICANT: ZHANG, LIANHUI
; TITLE OF INVENTION: CONTROL OF LEAF SCALD DISEASE

```

; FILE REFERENCE: 8795-13
; CURRENT APPLICATION NUMBER: US/09/029,785B
; CURRENT FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: PCT/AU96/00554
; EARLIER FILING DATE: 1996-09-06
; EARLIER APPLICATION NUMBER: AUSTRALIAN PN5278
; EARLIER FILING DATE: 1995-09-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Klebsiella oxytoca
US-09-029-785-6

Query Match 30.5%; Score 25; DB 4; Length 16;
Best Local Similarity 36.4%; Pred. No. 6.8e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 FPKLKVEVFPP 14
| : ::| ||
Db 6 FSQQELQVLPP 16

RESULT 47

US-09-500-124-181

; Sequence 181, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999

; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-181

Query Match 30.5%; Score 25; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFPK 6
||||
Db 5 PFPK 8

RESULT 48

US-09-500-124-239

; Sequence 239, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 239:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-239

```

```

Query Match          30.5%; Score 25; DB 4; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.8e+02;
Matches      5; Conservative      1; Mismatches      5; Indels      0; Gaps      0;

```

```

Qy      1 LKPFPKLKVEV 11
        | | | : | |
Db      6 LPPIPQSKTSV 16

```

```

RESULT 49
US-09-489-847-252
; Sequence 252, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 252
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-252

```


Query Match 30.5%; Score 25; DB 4; Length 16;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

Qy. 2 KPFPKLKVEVFPFP 15
:| | ||: || ||
Db 1 RPRP-LKLSVF-FP 12

RESULT 50

US-08-974-549A-163

; Sequence 163, Application US/08974549A

; Patent No. 6166178

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,549A

; FILING DATE: 19-NOV-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/911,312

```

; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-549A-163

```

```

Query Match          30.5%; Score 25; DB 3; Length 18;
Best Local Similarity 55.6%; Pred. No. 7.7e+02;
Matches      5; Conservative      1; Mismatches      3; Indels      0; Gaps      0;

```

```

Qy      3 PFPKLVKEV 11
        | | |:||
Db      9 PIKKEKIEV 17

```

```

Search completed: July 4, 2004, 04:48:51
Job time : 10.403 secs

```

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:35:16 ; Search time 11.5299 Seconds
 (without alignments)
 125.142 Million cell updates/sec

Title: US-09-641-802-8
 Perfect score: 82
 Sequence: 1 LKPFPLKVEVFPFP 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2898

Minimum DB seq length: 7
 Maximum DB seq length: 18

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	33	40.2	18	2	A60915
2	24	29.3	17	2	S78756
3	23.5	28.7	18	2	S04229
4	23	28.0	9	2	PC7073
5	22	26.8	13	2	C53275
6	22	26.8	17	2	G85956
7	22	26.8	18	2	A42576
8	22	26.8	18	2	A61220
9	21.5	26.2	16	2	A48301
10	21	25.6	8	2	S66646
11	21	25.6	11	1	XASNBA
12	21	25.6	15	2	PS0452
13	21	25.6	15	2	PA0060

enkephalin-degradi
 ribosomal protein
 N4-(beta-N-acetyl
 ubiquinol-cytochro
 Ig kappa-1 chain J
 hypothetical prote
 steroid receptor c
 epsilon receptor m
 glutamate-1-semial
 cardioacceleratory
 bradykinin-potenti
 32K protein 3306 -
 protein QF200037 -

14	21	25.6	16	2	I40065	shikimate 5-dehydr
15	21	25.6	16	2	PH0758	T-cell receptor be
16	20.5	25.0	14	2	H64008	hypothetical prote
17	20	24.4	10	2	A60624	angiotensin I - Ja
18	20	24.4	10	2	A60410	beta-neoendorphin
19	20	24.4	10	2	A90917	angiotensin precur
20	20	24.4	10	2	A90345	angiotensin precur
21	20	24.4	11	2	S07207	Crinia-angiotensin
22	20	24.4	11	2	PA0028	protein QA300042 -
23	20	24.4	13	2	S32475	lymnaDFamide 5 - g
24	20	24.4	14	2	PH1566	cerebrin 30 - huma
25	20	24.4	15	1	LFECF	phe operon leader
26	20	24.4	15	2	PA0026	protein QA300027 -
27	20	24.4	15	2	PA0024	protein QA300050 -
28	20	24.4	15	2	PA0088	protein QF200051 -
29	20	24.4	15	2	PD0444	coupling factor 6
30	20	24.4	16	2	A53337	regulatory protein
31	20	24.4	17	2	A37823	dihydrolipoamide S
32	20	24.4	18	2	S14661	photosystem I prot
33	20	24.4	18	2	S09731	photosystem I prot
34	20	24.4	18	2	A61392	brain-associated s
35	20	24.4	18	2	H75063	hypothetical prote
36	19	23.2	9	2	S66635	alpha-2-macroglobu
37	19	23.2	10	2	S65432	angiotensin I - ho
38	19	23.2	10	2	A61218	alpha-gliadin 4Ha
39	19	23.2	10	2	B61218	alpha-gliadin 6Ha
40	19	23.2	12	2	C20907	Ig kappa-1 chain J
41	19	23.2	13	2	S32474	lymnaDFamide 4 - g
42	19	23.2	14	2	A01250	angiotensin precur
43	19	23.2	15	2	A60834	angiotensin I prec
44	19	23.2	15	2	S29207	avenin gamma-4 - o
45	19	23.2	15	2	C61511	milk band B protei
46	19	23.2	16	2	A20190	hypodermin B - ear
47	19	23.2	16	2	S33590	beta-crystallin A3
48	19	23.2	18	2	PN0149	beta-Gliadine 13 -
49	18.5	22.6	17	2	S59481	hydroxyproline-ric
50	18	22.0	8	2	A46306	spasmogenic toxin
51	18	22.0	9	2	I46023	growth hormone rec
52	18	22.0	10	2	S74147	glyceraldehyde-3-p
53	18	22.0	11	2	S33519	probable secreted
54	18	22.0	11	2	S78026	ribosomal protein
55	18	22.0	11	2	PC2254	cytochrome P450 3A
56	18	22.0	12	2	PA0098	ribosomal protein
57	18	22.0	12	2	PH1567	cerebrin 28 - huma
58	18	22.0	13	2	S21152	tryptophyllin-rela
59	18	22.0	13	2	A60458	protocatechuate 3,
60	18	22.0	13	2	B44957	protein L7 - commo
61	18	22.0	13	2	S23640	Ig kappa chain J s
62	18	22.0	15	2	E91061	hypothetical prote
63	18	22.0	15	2	A28965	ribulose-bisphosph
64	18	22.0	16	2	D45193	zinc finger protei
65	18	22.0	17	2	S29165	quinaldine oxidore
66	18	22.0	17	2	I55612	thyroid hormone re
67	17.5	21.3	15	2	A41436	alpha-macroglobuli
68	17	20.7	9	2	S35538	ribosomal protein
69	17	20.7	9	2	A44873	caldesmon - rabbit
70	17	20.7	10	1	XASNPC	angiotensin-conver

71	17	20.7	10	2	JC1367	thyroliberin poten
72	17	20.7	10	2	B33143	pneumadin - human
73	17	20.7	10	2	A33143	pneumadin - rat
74	17	20.7	10	2	A60476	S-layer protein -
75	17	20.7	10	2	H28027	protein P11 - curl
76	17	20.7	11	2	G42762	proteasome endopep
77	17	20.7	11	2	S23306	substance P - Atla
78	17	20.7	11	2	A61033	ranatachykinin A -
79	17	20.7	11	2	D61033	ranatachykinin D -
80	17	20.7	12	2	S17869	glutathione transf
81	17	20.7	12	2	S65409	histone H2B - huma
82	17	20.7	12	2	A60757	enterotoxin C-1 -
83	17	20.7	12	2	A20907	Ig kappa chain J1
84	17	20.7	13	2	H64124	hypothetical prote
85	17	20.7	13	2	S32472	lymnaDFamide 2 - g
86	17	20.7	13	2	S23638	Ig kappa chain J s
87	17	20.7	14	2	C33098	223K exoantigen -
88	17	20.7	16	2	E58503	superoxide dismuta
89	17	20.7	16	2	T44936	calmodulin kinase
90	17	20.7	17	2	C37520	glutathione transf
91	17	20.7	17	2	S50901	chlorophyll a/b-bi
92	17	20.7	17	2	S33609	extensin - maize (
93	17	20.7	17	2	C49255	T-cell receptor be
94	17	20.7	17	2	PC2319	proteasome endopep
95	17	20.7	18	2	A45138	arsenite oxidase I
96	17	20.7	18	2	B35910	neurofibromatosis-
97	17	20.7	18	2	I78841	thrombopoietin rec
98	16.5	20.1	9	2	A61620	locustamyotropin I
99	16.5	20.1	15	2	S10891	ubiquitin thiolest
100	16.5	20.1	15	2	B61457	alpha-glucosidase

ALIGNMENTS

RESULT 1

A60915

enkephalin-degrading aminopeptidase (EC 3.4.-.-), puromycin-sensitive - rat (fragment)

N;Alternate names: aminoenkephalinase; aminopeptidase MII

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000

C;Accession: A60915

R;Dyer, S.H.; Slaughter, C.A.; Orth, K.; Moomaw, C.R.; Hersh, L.B.
J. Neurochem. 54, 547-554, 1990

A;Title: Comparison of the soluble and membrane-bound forms of the puromycin-sensitive enkephalin-degrading aminopeptidases from rat.

A;Reference number: A60915; MUID:90132681; PMID:2299352

A;Accession: A60915

A;Molecule type: protein

A;Residues: 1-18 <DYE>

A;Note: this sequence represents the N-terminus of both soluble and membrane-associated forms

C;Superfamily: membrane alanyl aminopeptidase

C;Keywords: hydrolase

Query Match

40.2%; Score 33; DB 2; Length 18;

Best Local Similarity 50.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KPFPKCLKVEVFP 13
:|| :| || |
Db 4 RPFERLPTEVSP 15

RESULT 2

S78756

ribosomal protein MRP-L5, mitochondrial - bovine (fragments)

C;Species: Bos primigenius taurus (cattle)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C;Accession: S78756

R;Graack, H.R.

submitted to the Protein Sequence Database, May 1999

A;Reference number: S78756

A;Accession: S78756

A;Molecule type: protein

A;Residues: 1-12;13-17 <GRA>

C;Keywords: mitochondrion

Query Match 29.3%; Score 24; DB 2; Length 17;
Best Local Similarity 62.5%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKCLKVE 10
|| |:||
Db 3 PFELLEVE 10

RESULT 3

S04229

N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24K chain - rat (fragment)

N;Alternate names: glycosylasparaginase

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993

C;Accession: S04229

R;Tollersrud, O.K.; Aronson Jr., N.N.

Biochem. J. 260, 101-108, 1989

A;Title: Purification and characterization of rat liver glycosylasparaginase.

A;Reference number: S04228; MUID:89374025; PMID:2775174

A;Accession: S04229

A;Molecule type: protein

A;Residues: 1-18 <TOL>

C;Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase

C;Keywords: hydrolase

Query Match 28.7%; Score 23.5; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 3 PFPKCLKVEVFPF 14
| | | | :||
Db 3 PLP-LVVNTWPF 13

RESULT 4

PC7073

ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 03-Jun-2002

C;Accession: PC7073

R;Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.; Morimasa, T.; Hosokawa, K.; Toda, T.

Electrophoresis 21, 1853-1871, 2000

A;Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of tissue proteins during the course of aging.

A;Reference number: PC7072

A;Accession: PC7073

A;Molecule type: protein

A;Residues: 1-9 <TSU>

C;Keywords: brain; core protein; oxidoreductase

Query Match 28.0%; Score 23; DB 2; Length 9;
Best Local Similarity 62.5%; Pred. No. 2.8e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKPFPLK 8
|| ||:
Db 2 LKVAPVK 9

RESULT 5

C53275

Ig kappa-1 chain J3 segment b95 allotype - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996

C;Accession: C53275

R;Ayadi, H.; Marche, P.N.; Cazenave, P.A.

Immunogenetics 34, 201-207, 1991

A;Title: Evolution of the rabbit immunoglobulin kappa chain genes.

A;Reference number: A53275; MUID:91372868; PMID:1909995

A;Accession: C53275

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-13 <AYA>

A;Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBIP:56164)

C;Comment: This J3 segment may not be functional because of substitutions in the 7 mer and 9 mer elements.

C;Keywords: heterotetramer; immunoglobulin

Query Match 26.8%; Score 22; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEVFP 13
| |:
Db 5 PGTKLEIKP 13

RESULT 6

G85956

hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C;Accession: G85956

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.; Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca, J.; Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.
Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: G85956

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-17 <STO>

A;Cross-references: GB:AE005174; NID:g12517539; PIDN:AAG58115.1; GSPDB:GN00145; UWGP:Z4331

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: Z4331

Query Match 26.8%; Score 22; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 VFPPF 15
| |||
Db 4 VSPFP 8

RESULT 7

A42576

steroid receptor complex Hsp56 60K component - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998

C;Accession: A42576

R;Yem, A.W.; Tomasselli, A.G.; Heinrichson, R.L.; Zurcher-Neely, H.; Ruff, V.A.; Johnson, R.A.; Deibel Jr., M.R.
J. Biol. Chem. 267, 2868-2871, 1992

A;Title: The Hsp56 component of steroid receptor complexes binds to immobilized FK506 and shows homology to FKBP-12 and FKBP-13.

A;Reference number: A42576; MUID:92147620; PMID:1371107

A;Accession: A42576

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <YEM>

A;Experimental source: thymus

A;Note: sequence extracted from NCBI backbone (NCBIP:80696)

C;Superfamily: human FK506-binding protein FKBP51; BKBP-type peptidylprolyl isomerase homology; tetratricopeptide repeat homology

C;Keywords: steroid hormone receptor

Query Match 26.8%; Score 22; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KVEVFPF 14
 :||:| |
 Db 11 EVELFEF 17

RESULT 8

A61220

epsilon receptor modulating protein (EC 3.4.21.-) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Mar-1996

C;Accession: A61220

R;Matsushita, S.; Katz, D.H.

Cell. Immunol. 137, 252-259, 1991

A;Title: The murine epsilon receptor modulating protein: a novel serine protease which modulates CD23 binding of IgE.

A;Reference number: A61220; MUID:91356570; PMID:1679381

A;Accession: A61220

A;Molecule type: protein

A;Residues: 1-18 <MAT>

C;Comment: This serine proteinase from a T cell hybridoma does not reduce levels of CD23, the low affinity IgE binding protein on B cells, but reduces the avidity of CD23 for IgE.

C;Keywords: hydrolase; serine proteinase

Query Match 26.8%; Score 22; DB 2; Length 18;

Best Local Similarity 80.0%; Pred. No. 2.1e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KPFFPK 6

|| ||

Db 2 KPAPK 6

RESULT 9

A48301

glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - Synechococcus sp. (PCC 6301) (fragment)

C;Species: Synechococcus sp.

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993

C;Accession: A48301

R;Grimm, B.; Bull, A.; Welinder, K.G.; Gough, S.P.; Kannangara, C.G.

Carlsberg Res. Commun. 54, 67-79, 1989

A;Title: Purification and partial amino acid sequence of the glutamate 1-semialdehyde aminotransferase of barley and synechococcus.

A;Reference number: A48301; MUID:89374545; PMID:2505791

A;Accession: A48301

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <GRI>

C;Keywords: intramolecular transferase; isomerase

Query Match 26.2%; Score 21.5; DB 2; Length 16;

Best Local Similarity 38.5%; Pred. No. 2.3e+03;

Matches 5; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy 1 LKPFPPKLKV-EVF 12
: || :| |:|
Db 3 INPFKTIKSDEIF 15

RESULT 10

S66646

cardioacceleratory protein 2b - tobacco hornworm

C;Species: Manduca sexta (tobacco hornworm)

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S66646

R;Huesmann, G.R.; Cheung, C.C.; Loi, P.K.; Lee, T.D.; Swiderek, K.M.; Tublitz, N.J.

FEBS Lett. 371, 311-314, 1995

A;Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide from the tobacco hawkmoth Manduca sexta.

A;Reference number: S66646; MUID:96013159; PMID:7556618

A;Accession: S66646

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <HUE>

Query Match 25.6%; Score 21; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 10 EVFPPF 15
|::||
Db 1 ELYAFP 6

RESULT 11

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995

C;Accession: A01254

R;Kato, H.; Suzuki, T.

Proc. Jpn. Acad. 46, 176-181, 1970

A;Reference number: A01254

A;Accession: A01254

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of a peptide having the identical structure and biological properties

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.6%; Score 21; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKPFPPKL 7
| | ||:
Db 3 LPPRPKI 9

RESULT 12

PS0452

32K protein 3306 - rice (strain Nihonbare) (fragment)

C;Species: *Oryza sativa* (rice)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995

C;Accession: PS0452

R;Tsugita, A.; Miyatake, N.

submitted to JIPID, April 1993

A;Reference number: PS0208

A;Accession: PS0452

A;Molecule type: protein

A;Residues: 1-15 <TSU>

A;Experimental source: bran, strain Nihonbare

C;Comment: molecular weight 32K, pI 5.3.

Query Match 25.6%; Score 21; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKL 7
| | | |
Db 6 PFPIL 10

RESULT 13

PA0060

protein QF200037 - fungus (*Fusarium sporotrichioides*) (fragment)

C;Species: *Fusarium sporotrichioides*

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C;Accession: PA0060

R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides* proteins.

A;Reference number: PA0051

A;Accession: PA0060

A;Molecule type: protein

A;Residues: 1-15 <CHO>

Query Match 25.6%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKPFPK 6
| : | | :
Db 2 LRPLPE 7

RESULT 14

I40065

shikimate 5-dehydrogenase (EC 1.1.1.25) - *Buchnera aphidicola* (fragment)

C;Species: *Buchnera aphidicola*

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999

C;Accession: I40065

R;Rouhbakhsh, D.; Baumann, P.

Gene 155, 107-112, 1995

A;Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding gene.

A;Reference number: I40061; MUID:95212914; PMID:7535281

A;Accession: I40065

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-16 <RES>

A;Cross-references: EMBL:U10499; NID:g854717; PIDN:AAA79128.1; PID:g854718

C;Genetics:

A;Gene: aroE

C;Keywords: oxidoreductase

Query Match 25.6%; Score 21; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPKLK 8
|||::
Db 9 FPKIE 13

RESULT 15

PH0758

T-cell receptor beta chain (E22) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C;Accession: PH0758

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-restricted cytotoxic T lymphocyte clones specific for a Plasmodium berghei nonapeptide: implications for T cell allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0758

A;Molecule type: mRNA

A;Residues: 1-16 <CAS>

A;Cross-references: EMBL:X60853; NID:g50743; PIDN:CAA43243.1; PID:g50744

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 25.6%; Score 21; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PFPKLKVEVF 12
| | |||
Db 5 PTGKSNTTEVF 14

RESULT 16

H64008

hypothetical protein HI0492 - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998

C;Accession: H64008

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.

A;Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: H64008

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-14 <TIGR>

A;Cross-references: GB:U32731; GB:L42023; NID:g1573465; PID:g1573478; TIGR:HI0492

Query Match 25.0%; Score 20.5; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 1 LKP-FPKL 7
:| | :| |:
Db 1 MKPKYPKM 8

RESULT 17

A60624

angiotensin I - Japanese quail

C;Species: *Coturnix coturnix japonica* (Japanese quail)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 15-Sep-2003

C;Accession: A60624

R;Takei, Y.; Hasegawa, Y.

Gen. Comp. Endocrinol. 79, 12-22, 1990

A;Title: Vasopressor and depressor effects of native angiotensins and inhibition of these effects in the Japanese quail.

A;Reference number: A60624; MUID:90284684; PMID:2191893

A;Accession: A60624

A;Molecule type: protein

A;Residues: 1-10 <TAK>

C;Superfamily: Serpin

C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 24.4%; Score 20; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KVEVFPF 14
:| | | |
Db 2 RVYVHPF 8

RESULT 18

A60410

beta-neoendorphin / dynorphin precursor - guinea pig
N;Alternate names: alpha-neoendorphin; proenkephalin B precursor
C;Species: Cavia porcellus (guinea pig)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 21-Jan-2000
C;Accession: A60410
R;Murphy, R.; Turner, C.A.
Peptides 11, 65-68, 1990
A;Title: Isolation and microsequence analysis of guinea pig alpha-neo-endorphin.
A;Reference number: A60410; MUID:90259864; PMID:2342991
A;Accession: A60410
A;Molecule type: protein
A;Residues: 1-10 <MUR>
C;Superfamily: proenkephalin
C;Keywords: neuropeptide; opioid peptide

Query Match 24.4%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKPFPPK 6
| : ||
Db 5 LRKYPK 10

RESULT 19

A90917

angiotensin precursor - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998

C;Accession: A90917; A01250

R;Nakayama, T.; Nakajima, T.; Sokabe, H.

Chem. Pharm. Bull. 21, 2085-2087, 1973

A;Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its identification by DNS-method.

A;Reference number: A90917; MUID:74127845; PMID:4361802

A;Accession: A90917

A;Molecule type: protein

A;Residues: 1-10 <NAK>

C;Keywords: blood pressure control; hormone; vasoconstrictor

F;1-10/Product: angiotensin I #status experimental <AN1>

F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 24.4%; Score 20; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KVEVFPPF 14
: | | ||
Db 2 RVYVHPF 8

RESULT 20

A90345

angiotensin precursor - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998

C;Accession: A90345; A01250

R;Elliott, D.F.; Peart, W.S.
Biochem. J. 65, 246-254, 1957
A;Title: The amino acid sequence in a hypertensin.
A;Reference number: A90345
A;Accession: A90345
A;Molecule type: protein
A;Residues: 1-10 <ELL>
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 24.4%; Score 20; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KVEVFPP 14
:| | |
Db 2 RVYVHPF 8

RESULT 21

S07207

Crinia-angiotensin, skin - frog (*Crinia georgiana*)
C;Species: *Crinia georgiana*
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Aug-2000
C;Accession: S07207
R;Erspamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.
Experientia 35, 1132-1133, 1979
A;Title: Amino acid composition and sequence of crinia-angiotensin, an
angiotensin II-like endecapeptide from the skin of the Australian frog *Crinia*
georgiana.
A;Reference number: S07207; MUID:80024575; PMID:488254
A;Accession: S07207
A;Molecule type: protein
A;Residues: 1-11 <ERS>
C;Superfamily: unassigned animal peptides

Query Match 24.4%; Score 20; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PKLKVEVFPP 14
| :: | |
Db 2 PGDRIYVHPF 11

RESULT 22

PA0028

protein QA300042 - *Arabidopsis thaliana* (fragment)
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0028
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of *Arabidopsis* proteins by two-
dimensional gel electrophoresis.
A;Reference number: PA0001

A;Accession: PA0028
A;Molecule type: protein
A;Residues: 1-11 <KAM>
A;Experimental source: seed
C;Keywords: seed

Query Match 24.4%; Score 20; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5
|||
Db 6 PFP 8

RESULT 23

S32475

lymnaDFamide 5 - great pond snail

C;Species: *Lymnaea stagnalis* (great pond snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999

C;Accession: S32475

R;Johnsen, A.H.; Rehfeld, J.F.

Eur. J. Biochem. 213, 875-879, 1993

A;Title: LymnaDFamides, a new family of neuropeptides from the pond snail, *Lymnaea stagnalis*. Clue to cholecystokinin immunoreactivity in invertebrates?

A;Reference number: S32471; MUID:93238777; PMID:8477756

A;Accession: S32475

A;Molecule type: protein

A;Residues: 1-13 <JOH>

A;Cross-references: PIDN:AAB26366.1; PID:g299833

A;Experimental source: ganglia

C;Keywords: amidated carboxyl end; neuropeptide

F;13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 24.4%; Score 20; DB 2; Length 13;
Best Local Similarity 30.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PFPKLKVEVF 12
|| :: |
Db 1 PFDRISSSAF 10

RESULT 24

PH1566

cerebrin 30 - human (fragment)

C;Species: *Homo sapiens* (man)

C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999

C;Accession: PH1566

R;Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.
J. Neurochem. 61, 533-540, 1993

A;Title: Micropurification of two human cerebrospinal fluid proteins by high performance electrophoresis chromatography.

A;Reference number: PH1566; MUID:93329419; PMID:8336140

A;Accession: PH1566

A;Molecule type: protein

A;Residues: 1-14 <LEO>

Query Match 24.4%; Score 20; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 3.6e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEVFP 13
|: :| | |
Db 2 PEAQVSVQP 10

RESULT 25

LFECF

phe operon leader peptide - Escherichia coli (strain K-12)

N;Alternate names: attenuator peptide

C;Species: Escherichia coli

C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 01-Mar-2002

C;Accession: A03593; B36494; A65038

R;Zurawski, G.; Brown, K.; Killingly, D.; Yanofsky, C.

Proc. Natl. Acad. Sci. U.S.A. 75, 4271-4275, 1978

A;Title: Nucleotide sequence of the leader region of the phenylalanine operon of Escherichia coli.

A;Reference number: A03593; MUID:79033820; PMID:360214

A;Accession: A03593

A;Molecule type: DNA

A;Residues: 1-15 <ZUR>

A;Cross-references: GB:V00314; GB:J01658; NID:g42378; PIDN:CAA23600.1; PID:g42379

R;Gavini, N.; Davidson, B.E.

J. Biol. Chem. 265, 21532-21535, 1990

A;Title: pheA mutants of Escherichia coli have a defective pheA attenuator.

A;Reference number: A36494; MUID:91072346; PMID:2254312

A;Accession: B36494

A;Molecule type: DNA

A;Residues: 1-15 <GAV>

A;Cross-references: GB:M58024; GB:J05694; NID:g147178; PIDN:AAA62783.1; PID:g147180

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: A65038

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-15 <BLAT>

A;Cross-references: GB:AE000346; GB:U00096; NID:g2367141; PIDN:AAC75647.1; PID:g1788950; UWGP:b2598

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: pheL; pheAe

A;Map position: 56 min

C;Superfamily: pheA leader peptide

Query Match 24.4%; Score 20; DB 1; Length 15;
Best Local Similarity 33.3%; Pred. No. 3.9e+03;
Matches 5; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVFPP 15
:| | |
Db 1 MKHIPFFFAFFFTFP 15

RESULT 26

PA0026

protein QA300027 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0026
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis.
A;Reference number: PA0001
A;Accession: PA0026
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Experimental source: leaf

Query Match 24.4%; Score 20; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 3.9e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LKVEVFPP 14
||| ||
Db 2 LKVYGXPF 9

RESULT 27

PA0024

protein QA300050 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0024
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis.
A;Reference number: PA0001
A;Accession: PA0024
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Experimental source: seed

Query Match 24.4%; Score 20; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5
|||
Db 6 PFP 8

RESULT 28

PA0088

protein QF200051 - fungus (*Fusarium sporotrichioides*) (fragment)

C;Species: *Fusarium sporotrichioides*

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C;Accession: PA0088

R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides* proteins.

A;Reference number: PA0051

A;Accession: PA0088

A;Molecule type: protein

A;Residues: 1-15 <CHO>

Query Match 24.4%; Score 20; DB 2; Length 15;
Best Local Similarity 27.3%; Pred. No. 3.9e+03;
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PKLKVEVFPFP 15
| : : : | |
Db 3 PDIPXDDYPAP 13

RESULT 29

PD0444

coupling factor 6 mitochondrial - mouse (fragment)

C;Species: *Mus musculus* (house mouse)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999

C;Accession: PD0444

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.
submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Contents: Striatum

A;Accession: PD0444

A;Molecule type: protein

A;Residues: 1-15 <KAW>

C;Keywords: mitochondrion

Query Match 24.4%; Score 20; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.9e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LKPFPPKLKVE 10
| | || | :
Db 4 LDPVQKLFVD 13

RESULT 30

A53337

regulatory protein tyrR - *Escherichia coli* (fragment)

C;Species: *Escherichia coli*

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 07-May-1999

C;Accession: A53337

R;Argaet, V.P.; Wilson, T.J.; Davidson, B.E.

J. Biol. Chem. 269, 5171-5178, 1994

A;Title: Purification of the Escherichia coli regulatory protein TyrR and analysis of its interactions with ATP, tyrosine, phenylalanine, and tryptophan.
A;Reference number: A53337; MUID:94148980; PMID:8106498
A;Accession: A53337
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <ARG>

Query Match 24.4%; Score 20; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LKVEVF 12
::|||
Db 1 MRLEVF 6

RESULT 31

A37823

dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-May-2000

C;Accession: A37823

R;Rahmatullah, M.; Radke, G.A.; Andrews, P.C.; Roche, T.E.

J. Biol. Chem. 265, 14512-14517, 1990

A;Title: Changes in the core of the mammalian-pyruvate dehydrogenase complex upon selective removal of the lipoyl domain from the transacetylase component but not from the protein X component.

A;Reference number: A37823; MUID:90354445; PMID:2167319

A;Accession: A37823

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-17 <RAH>

C;Keywords: acyltransferase; coenzyme A

Query Match 24.4%; Score 20; DB 2; Length 17;
Best Local Similarity 55.6%; Pred. No. 4.4e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEVFP 13
||:| | |
Db 2 PKGRVFPVSP 10

RESULT 32

S14661

photosystem I protein psaA - maize (fragment)

C;Species: Zea mays (maize)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999

C;Accession: S14661

R;Kangasjarvi, J.; Gengenbach, B.G.

submitted to the EMBL Data Library, March 1991

A;Description: Nucleotide sequence of maize plastid genome BamHI 14 fragment.

A;Reference number: S14660

A;Accession: S14661

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-18 <KAN>

A;Cross-references: EMBL:X58080; NID:g12429; PIDN:CAA41109.1; PID:g12431

C;Superfamily: photosystem I P700 apoprotein

Query Match 24.4%; Score 20; DB 2; Length 18;
Best Local Similarity 42.9%; Pred. No. 4.7e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PKLKVEV 11
|::|: |
Db 8 PEVKIAV 14

RESULT 33

S09731

photosystem I protein psaI - spinach chloroplast (fragment)

C;Species: chloroplast Spinacia oleracea (spinach)

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 19-Jan-1996

C;Accession: S09731

R;Ikeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.

FEBS Lett. 263, 274-278, 1990

A;Title: Polypeptide composition of higher plant photosystem I complex.

Identification of psaI, psaJ and psaK gene products.

A;Reference number: S09730; MUID:90242987; PMID:2185953

A;Accession: S09731

A;Molecule type: protein

A;Residues: 1-18 <IKE>

C;Genetics:

A;Gene: psaI

A;Genome: chloroplast

C;Superfamily: photosystem I protein psaI

C;Keywords: chloroplast; membrane-associated complex; photosynthesis;
photosystem I; thylakoid

Query Match 24.4%; Score 20; DB 2; Length 18;
Best Local Similarity 42.9%; Pred. No. 4.7e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

Qy 4 FPKLKVE---VFP 13
|| : | |||
Db 3 FPSIFVPLVGLVFP 16

RESULT 34

A61392

brain-associated small cell lung cancer antigen - human (fragment)

N;Alternate names: BASCA

C;Species: Homo sapiens (man)

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Sep-1994

C;Accession: A61392

R;Umezawa, Y.; Kuge, S.; Kikyo, N.; Shirai, T.; Watanabe, J.; Fujiwara, M.;
Okabe, T.

Jpn. J. Clin. Oncol. 21, 251-255, 1991

A;Title: Identity of brain-associated small cell lung cancer antigen and the
CD56 (NKH-1/Leu-19) leukocyte differentiation antigen and the neural cell
adhesion molecule.

A;Reference number: A61392; MUID:92046737; PMID:1719260

A;Accession: A61392
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <UME>

Query Match 24.4%; Score 20; DB 2; Length 18;
Best Local Similarity 42.9%; Pred. No. 4.7e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 7 LKVEVFP 13
|:|::|
Db 1 LQVDIVP 7

RESULT 35

H75063

hypothetical protein PAB7382 - *Pyrococcus abyssi* (strain Orsay)

C;Species: *Pyrococcus abyssi*

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C;Accession: H75063

R;anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome structure and evolution.

A;Reference number: A75001

A;Accession: H75063

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-18 <KAW>

A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50405.1;

PID:el516303; PID:g5458918

A;Experimental source: strain Orsay

C;Genetics:

A;Gene: PAB7382

Query Match 24.4%; Score 20; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLKVE 10
||:||
Db 2 KLRVE 6

RESULT 36

S66635

alpha-2-macroglobulin isoform 1 - bovine (fragment)

C;Species: *Bos primigenius indicus* (zebu cattle)

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S66635

R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottrup-Jensen, L.; Nyborg, J.

FEBS Lett. 372, 93-95, 1995

A;Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain of human and bovine alpha(2)-macroglobulin.

A;Reference number: S66634; MUID:96032553; PMID:7556651

A;Accession: S66635

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <DOL>

Query Match 23.2%; Score 19; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 FPF 14
|||
Db 4 FPF 6

RESULT 37

S65432

angiotensin I - horn fly (fragment)

C;Species: Haematobia irritans (horn fly)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C;Accession: S65432

R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.;
Willadsen, P.

Eur. J. Biochem. 237, 414-423, 1996

A;Title: Cloning and characterisation of angiotensin-converting enzyme from the
dipteran species, Haematobia irritans exigua, and its expression in the maturing
male reproductive system.

A;Reference number: S65431; MUID:96215437; PMID:8647080

A;Accession: S65432

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <WIJ>

A;Note: the source is designated as Haematobia irritans exigua

Query Match 23.2%; Score 19; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KVEVFPPF 14
:| : ||
Db 2 RVYIHPF 8

RESULT 38

A61218

alpha-gliadin 4Ha - grass (Haynaldia villosa) (fragment)

C;Species: Haynaldia villosa, Dasypyrum villosum

C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999

C;Accession: A61218

R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafiandra, D.

Biochem. Genet. 29, 207-211, 1991

A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of
Haynaldia villosa Schur (syn. Dasypyrum villosum L.).

A;Reference number: A61218; MUID:91315394; PMID:1859356

A;Accession: A61218

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <SHE>

C;Keywords: seed; storage protein

Query Match 23.2%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLLK 8
| | : | :
Db 5 PVPQLQ 10

RESULT 39

B61218

alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)

C;Species: Haynaldia villosa, Dasypyrum villosum

C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999

C;Accession: B61218

R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafiandra, D.

Biochem. Genet. 29, 207-211, 1991

A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa Schur (syn. Dasypyrum villosum L.).

A;Reference number: A61218; MUID:91315394; PMID:1859356

A;Accession: B61218

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <SHE>

C;Keywords: seed; storage protein

Query Match 23.2%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLLK 8
| | : | :
Db 4 PVPQLQ 9

RESULT 40

C20907

Ig kappa-1 chain J3 region - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 16-Aug-1996

C;Accession: C20907

R;Emorine, L.; Max, E.E.

Nucleic Acids Res. 11, 8877-8890, 1983

A;Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple deletions.

A;Reference number: A20907; MUID:84169523; PMID:6324107

A;Accession: C20907

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-12 <EMO>

C;Keywords: heterotetramer; immunoglobulin

Query Match 23.2%; Score 19; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 4.5e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LKPFPLKVE 10
| | ||:::
Db 3 LGPGTKLEIK 12

RESULT 41

S32474

lymnaDFamide 4 - great pond snail

C;Species: Lymnaea stagnalis (great pond snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999

C;Accession: S32474

R;Johnsen, A.H.; Rehfeld, J.F.

Eur. J. Biochem. 213, 875-879, 1993

A;Title: LymnaDFamides, a new family of neuropeptides from the pond snail, Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in invertebrates?

A;Reference number: S32471; MUID:93238777; PMID:8477756

A;Accession: S32474

A;Molecule type: protein

A;Residues: 1-13 <JOH>

A;Cross-references: PIDN:AAB26365.1; PID:g299832

A;Experimental source: ganglia

C;Keywords: amidated carboxyl end; neuropeptide

F;13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 23.2%; Score 19; DB 2; Length 13;
Best Local Similarity 30.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PFPKLKVEVF 12
|| :: |
Db 1 PFDRI NSAF 10

RESULT 42

A01250

angiotensin precursor - horse (fragment)

C;Species: Equus caballus (domestic horse)

C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 15-Sep-2003

C;Accession: A92775; A01250

R;Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.

J. Exp. Med. 106, 439-453, 1957

A;Reference number: A92775

A;Accession: A92775

A;Molecule type: protein

A;Residues: 1-14 <SKE>

C;Superfamily: Serpin

C;Keywords: blood pressure control; hormone; vasoconstrictor

F;1-10/Product: angiotensin I #status experimental <AN1>

F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 23.2%; Score 19; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 5.3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KVEVFPPF 14
:| : ||
Db 2 RVYIHPF 8

RESULT 43

A60834

angiotensin I precursor - dog (fragment)

N;Alternate names: angiotensinogen I

N;Contains: angiotensin I

C;Species: Canis lupus familiaris (dog)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Sep-2003

C;Accession: A60834

R;Oliver, J.A.

Hypertension 11, 21-27, 1988

A;Title: Purification and partial characterization of canine angiotensinogen.

A;Reference number: A60834; MUID:88113996; PMID:3338837

A;Accession: A60834

A;Molecule type: protein

A;Residues: 1-15 <OLI>

C;Superfamily: Serpin

C;Keywords: glycoprotein; plasma

F;1-10/Product: angiotensin I #status predicted <MAT>

Query Match 23.2%; Score 19; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 5.7e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KVEVFPF 14
:| : ||
Db 2 RVYIHPF 8

RESULT 44

S29207

avenin gamma-4 - oat (fragment)

N;Alternate names: CIP-1; coeliac immunoreactive protein 1

C;Species: Avena sativa (oat)

C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998

C;Accession: S29207

R;Rocher, A.; Colilla, F.; Ortiz, M.L.; Mendez, E.

FEBS Lett. 310, 37-40, 1992

A;Title: Identification of the three major coeliac immunoreactive proteins and one alpha-amylase inhibitor from oat endosperm.

A;Reference number: S29207; MUID:92405739; PMID:1526282

A;Accession: S29207

A;Molecule type: protein

A;Residues: 1-15 <ROC>

A;Experimental source: endosperm

C;Superfamily: gliadin

C;Keywords: prolamin; seed

Query Match 23.2%; Score 19; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KPFPK 6
:|:|:
Db 6 QPYPE 10

RESULT 45

C61511

milk band B protein - Australian echidna (fragment)

C;Species: Tachyglossus aculeatus (Australian echidna)

C;Date: 09-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000

C;Accession: C61511

R;Teahan, C.G.; McKenzie, H.A.; Griffiths, M.

Comp. Biochem. Physiol. B 99, 99-118, 1991

A;Title: Some monotreme milk "whey" and blood proteins.

A;Reference number: A61511; MUID:92070088; PMID:1959333

A;Accession: C61511

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <GRI>

C;Keywords: glycoprotein

Query Match 23.2%; Score 19; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 FPF 14
| | |
Db 13 FPF 15

RESULT 46

A20190

hypodermin B - early cattle grub (fragment)

C;Species: Hypoderma lineatum (early cattle grub)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Jun-1993

C;Accession: A20190

R;Lecroisey, A.; Tong, N.T.; Keil, B.

Eur. J. Biochem. 134, 261-267, 1983

A;Title: Hypodermin B, a trypsin-related enzyme from the insect Hypoderma lineatum.

A;Reference number: A20190; MUID:83261874; PMID:6307690

A;Accession: A20190

A;Molecule type: protein

A;Residues: 1-16 <LEC>

Query Match 23.2%; Score 19; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEVFPF 14
: | | |
Db 9 IEDFPW 14

RESULT 47

S33590

beta-crystallin A3 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999

C;Accession: S33590

R;David, L.L.; Shearer, T.R.

FEBS Lett. 324, 265-270, 1993

A;Title: beta-crystallins insolubilized by calpain II in vitro contain cleavage sites similar to beta-crystallins insolubilized during cataract.

A;Reference number: S33586; MUID:94009594; PMID:8405363

A;Accession: S33590

A;Molecule type: protein

A;Residues: 1-16 <DAV>

Query Match 23.2%; Score 19; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PKLKVE 10
| | | |
Db 3 PTTKVE 8

RESULT 48

PN0149

beta-Gliadine 13 - Aegilops longissima (fragment)

C;Species: Aegilops longissima

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PN0149

R;Odintsova, T.I.; Egorov, T.A.

Biokhimiia 55, 509-516, 1990

A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of polyploid wheat genomes.

A;Reference number: PN0146; MUID:90283493; PMID:2354218

A;Accession: PN0149

A;Molecule type: protein

A;Residues: 1-18 <ODI>

A;Experimental source: strain K-202

C;Superfamily: gliadin

Query Match 23.2%; Score 19; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLLK 8
| | | |
Db 4 PVPQLQ 9

RESULT 49

S59481

hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)

C;Species: Phaseolus vulgaris (kidney bean)

C;Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998

C;Accession: S59481

R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A;Title: Specificity in the immobilisation of cell wall proteins in response to different elicitor molecules in suspension-cultured cells of French bean (Phaseolus vulgaris L.).

A;Reference number: S59481; MUID:96011753; PMID:7548825

A;Accession: S59481

A;Molecule type: protein

A;Residues: 1-17 <WOJ>
C;Keywords: glycoprotein; hydroxyproline
F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 22.6%; Score 18.5; DB 2; Length 17;
Best Local Similarity 46.2%; Pred. No. 7.9e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Qy 1 LKPFPKLKVEVFP 13
| | | | |
Db 4 LPPVPPPPV-VYP 15

RESULT 50

A46306

spasmogenic toxin PNVI - spider (Phoneutria nigriventer) (fragment)

C;Species: Phoneutria nigriventer

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999

C;Accession: A46306

R;Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.;
Novello, J.C.; Domont, G.B.; Giglio, J.R.; Oliveira, B.; de Nucci, G.

Toxicon 31, 377-384, 1993

A;Title: Biochemical characterization of a vascular smooth muscle contracting
polypeptide purified from Phoneutria nigriventer (armed spider) venom.

A;Reference number: A46306; MUID:93276438; PMID:8503129

A;Accession: A46306

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <MAR>

Query Match 22.0%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 EVFP 13
| |
Db 1 EAFP 4

Search completed: July 4, 2004, 04:47:19

Job time : 11.5299 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:45:52 ; Search time 29.4403 Seconds
(without alignments)
158.601 Million cell updates/sec

Title: US-09-641-802-8
Perfect score: 82
Sequence: 1 LKPFPLKVEVFPFP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 203405

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query			Description
No.	Score	Match	Length	ID	

1	82	100.0	15	14	US-10-281-652-8	Sequence 8, Appli
2	37	45.1	18	9	US-09-864-761-40786	Sequence 40786, A
3	36	43.9	18	14	US-10-281-652-22	Sequence 22, Appl
4	34	41.5	15	14	US-10-281-652-5	Sequence 5, Appli
5	32	39.0	9	12	US-09-935-430-451	Sequence 451, App
6	32	39.0	9	12	US-09-935-430-555	Sequence 555, App
7	32	39.0	9	14	US-10-277-292-451	Sequence 451, App
8	32	39.0	9	14	US-10-277-292-555	Sequence 555, App
9	32	39.0	9	15	US-10-280-340-451	Sequence 451, App
10	32	39.0	9	15	US-10-280-340-555	Sequence 555, App
11	32	39.0	10	12	US-09-935-430-66	Sequence 66, Appl
12	32	39.0	10	12	US-09-935-430-607	Sequence 607, App
13	32	39.0	10	14	US-10-277-292-66	Sequence 66, Appl
14	32	39.0	10	14	US-10-277-292-607	Sequence 607, App
15	32	39.0	10	15	US-10-280-340-66	Sequence 66, Appl
16	32	39.0	10	15	US-10-280-340-607	Sequence 607, App
17	32	39.0	16	14	US-10-225-567A-1110	Sequence 1110, Ap
18	31	37.8	13	9	US-09-766-412-39	Sequence 39, Appl
19	30.5	37.2	18	14	US-10-226-007-1525	Sequence 1525, Ap
20	29	35.4	12	9	US-09-281-717-31	Sequence 31, Appl
21	29	35.4	12	9	US-09-281-717-33	Sequence 33, Appl
22	29	35.4	12	9	US-09-281-717-35	Sequence 35, Appl
23	28	34.1	9	12	US-09-935-430-333	Sequence 333, App
24	28	34.1	9	14	US-10-277-292-333	Sequence 333, App
25	28	34.1	9	15	US-10-280-340-333	Sequence 333, App
26	28	34.1	10	12	US-09-935-430-269	Sequence 269, App
27	28	34.1	10	12	US-09-935-430-356	Sequence 356, App
28	28	34.1	10	14	US-10-033-662-35	Sequence 35, Appl
29	28	34.1	10	14	US-10-277-292-269	Sequence 269, App
30	28	34.1	10	14	US-10-277-292-356	Sequence 356, App
31	28	34.1	10	15	US-10-280-340-269	Sequence 269, App
32	28	34.1	10	15	US-10-280-340-356	Sequence 356, App
33	28	34.1	14	9	US-09-918-171A-29	Sequence 29, Appl
34	28	34.1	16	9	US-09-947-124-5	Sequence 5, Appli
35	27	32.9	10	12	US-10-203-334-2	Sequence 2, Appli
36	27	32.9	10	12	US-10-601-837-131	Sequence 131, App
37	27	32.9	10	12	US-09-988-493-133	Sequence 133, App
38	27	32.9	10	12	US-10-014-340-427	Sequence 427, App
39	27	32.9	10	12	US-10-014-340-428	Sequence 428, App
40	27	32.9	11	14	US-10-100-049-25	Sequence 25, Appl
41	27	32.9	12	14	US-10-340-458-24	Sequence 24, Appl
42	27	32.9	14	12	US-10-308-128-144	Sequence 144, App
43	27	32.9	14	14	US-10-226-007-1513	Sequence 1513, Ap
44	27	32.9	15	10	US-09-774-639-257	Sequence 257, App
45	27	32.9	15	10	US-09-969-730-339	Sequence 339, App
46	27	32.9	15	12	US-10-682-420-80	Sequence 80, Appl
47	27	32.9	15	12	US-10-682-420-81	Sequence 81, Appl
48	27	32.9	15	14	US-10-226-007-1514	Sequence 1514, Ap
49	27	32.9	15	14	US-10-226-007-1516	Sequence 1516, Ap
50	27	32.9	15	16	US-10-621-363-339	Sequence 339, App
51	27	32.9	15	16	US-10-409-613-80	Sequence 80, Appl
52	27	32.9	15	16	US-10-409-613-81	Sequence 81, Appl
53	27	32.9	15	16	US-10-442-180-80	Sequence 80, Appl
54	27	32.9	15	16	US-10-442-180-81	Sequence 81, Appl
55	27	32.9	16	14	US-10-100-049-40	Sequence 40, Appl
56	27	32.9	16	14	US-10-226-007-1515	Sequence 1515, Ap

57	27	32.9	16	14	US-10-226-007-1517	Sequence 1517, Ap
58	27	32.9	16	14	US-10-226-007-1519	Sequence 1519, Ap
59	27	32.9	17	11	US-09-754-831A-34	Sequence 34, Appl
60	27	32.9	17	14	US-10-226-007-1518	Sequence 1518, Ap
61	27	32.9	17	14	US-10-226-007-1520	Sequence 1520, Ap
62	27	32.9	17	14	US-10-226-007-1522	Sequence 1522, Ap
63	27	32.9	18	14	US-10-226-007-1521	Sequence 1521, Ap
64	27	32.9	18	14	US-10-226-007-1523	Sequence 1523, Ap
65	26.5	32.3	13	9	US-09-030-619-93	Sequence 93, Appl
66	26.5	32.3	13	9	US-09-030-619-100	Sequence 100, App
67	26.5	32.3	13	12	US-10-277-232-93	Sequence 93, Appl
68	26.5	32.3	13	12	US-10-277-232-100	Sequence 100, App
69	26.5	32.3	13	14	US-10-229-368-8	Sequence 8, Appli
70	26.5	32.3	13	14	US-10-225-087-8	Sequence 8, Appli
71	26.5	32.3	13	15	US-10-277-233-93	Sequence 93, Appl
72	26.5	32.3	13	15	US-10-277-233-100	Sequence 100, App
73	26.5	32.3	13	15	US-10-351-985-22	Sequence 22, Appl
74	26.5	32.3	13	15	US-10-403-104-28	Sequence 28, Appl
75	26.5	32.3	13	15	US-10-403-104-29	Sequence 29, Appl
76	26	31.7	7	14	US-10-293-371-30	Sequence 30, Appl
77	26	31.7	7	14	US-10-293-371-32	Sequence 32, Appl
78	26	31.7	7	14	US-10-293-371-40	Sequence 40, Appl
79	26	31.7	7	14	US-10-293-371-41	Sequence 41, Appl
80	26	31.7	7	14	US-10-293-371-42	Sequence 42, Appl
81	26	31.7	9	10	US-09-865-548A-126	Sequence 126, App
82	26	31.7	10	10	US-09-572-270A-221	Sequence 221, App
83	26	31.7	11	15	US-10-367-405-5	Sequence 5, Appli
84	26	31.7	12	10	US-09-954-385-432	Sequence 432, App
85	26	31.7	12	14	US-10-100-049-31	Sequence 31, Appl
86	26	31.7	12	15	US-10-367-405-1	Sequence 1, Appli
87	26	31.7	12	15	US-10-367-405-2	Sequence 2, Appli
88	26	31.7	12	15	US-10-367-405-14	Sequence 14, Appl
89	26	31.7	12	16	US-10-070-406A-7	Sequence 7, Appli
90	26	31.7	14	14	US-10-145-206-29	Sequence 29, Appl
91	26	31.7	15	10	US-09-726-470A-224	Sequence 224, App
92	26	31.7	17	14	US-10-225-567A-2095	Sequence 2095, Ap
93	26	31.7	17	15	US-10-378-479-40	Sequence 40, Appl
94	26	31.7	18	14	US-10-251-703-33	Sequence 33, Appl
95	25	30.5	7	14	US-10-293-371-15	Sequence 15, Appl
96	25	30.5	9	12	US-09-935-430-452	Sequence 452, App
97	25	30.5	9	12	US-09-935-430-551	Sequence 551, App
98	25	30.5	9	14	US-10-292-418-15	Sequence 15, Appl
99	25	30.5	9	14	US-10-277-292-452	Sequence 452, App
100	25	30.5	9	14	US-10-277-292-551	Sequence 551, App

ALIGNMENTS

RESULT 1
 US-10-281-652-8
 ; Sequence 8, Application US/10281652
 ; Publication No. US20030091606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
 ; FILE REFERENCE: 265.00220101
 ; CURRENT APPLICATION NUMBER: US/10/281,652
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: US/09/641,803
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide
 US-10-281-652-8

Query Match 100.0%; Score 82; DB 14; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVFPFP 15
 |||||
 Db 1 LKPFPKLKVEVFPFP 15

RESULT 2

US-09-864-761-40786

; Sequence 40786, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
 USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aeomica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667

```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40786
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC023296.2
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
US-09-864-761-40786

```

```

Query Match          45.1%;   Score 37;   DB 9;   Length 18;
Best Local Similarity 75.0%;   Pred. No. 43;
Matches      6;   Conservative      1;   Mismatches      1;   Indels      0;   Gaps      0;

```

```

Qy      8 KVEVFPFP 15
        :|| |||
Db      3 RVEAFPPF 10

```

```

RESULT 3
US-10-281-652-22
; Sequence 22, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan

```

```

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-22

```

```

Query Match          43.9%; Score 36; DB 14; Length 18;
Best Local Similarity 70.0%; Pred. No. 62;
Matches      7; Conservative    0; Mismatches    3; Indels      0; Gaps      0;

```

```

Qy      3 PFPKLVVEVF 12
        ||||  || |
Db      5 PFPKYPVEPF 14

```

RESULT 4

US-10-281-652-5

```

; Sequence 5, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-5

```

Query Match 41.5%; Score 34; DB 14; Length 15;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEVFPP 14
| | || |||
Db 5 PVLPEVFPP 14

RESULT 5

US-09-935-430-451
; Sequence 451, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 451
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-451

Query Match 39.0%; Score 32; DB 12; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLKV 9
| |||||
Db 2 PMPKLKV 8

RESULT 6

US-09-935-430-555
; Sequence 555, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE

```

; APPLICANT:  RAITANO, ARTHUR
; APPLICANT:  AFAR, DANIEL
; APPLICANT:  LEVIN, ELANA
; APPLICANT:  CHALLITA-EID, PIA
; APPLICANT:  JAKOBOVITZ, AYA
; TITLE OF INVENTION:  NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION:  USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION:  OTHER CANCERS
; FILE REFERENCE:  51158-20050.00
; CURRENT APPLICATION NUMBER:  US/09/935,430
; CURRENT FILING DATE:  2001-08-22
; PRIOR APPLICATION NUMBER:  60/227,098
; PRIOR FILING DATE:  2000-08-22
; PRIOR APPLICATION NUMBER:  60/282,739
; PRIOR FILING DATE:  2001-04-10
; NUMBER OF SEQ ID NOS:  700
; SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 555
;   LENGTH:  9
;   TYPE:  PRT
;   ORGANISM:  Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION:  Description of Artificial Sequence:  Peptide motif
US-09-935-430-555

```

```

Query Match          39.0%;  Score 32;  DB 12;  Length 9;
Best Local Similarity 85.7%;  Pred. No. 1.2e+06;
Matches      6;  Conservative    0;  Mismatches    1;  Indels      0;  Gaps      0;

```

```

Qy          3 PFPKLVK 9
              | |||||
Db          2 PMPKLVK 8

```

RESULT 7

```

US-10-277-292-451
; Sequence 451, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT:  FARIS, MARY
; APPLICANT:  HUBERT, RENE
; APPLICANT:  RAITANO, ARTHUR
; APPLICANT:  AFAR, DANIEL
; APPLICANT:  LEVIN, ELANA
; APPLICANT:  CHALLITA-EID, PIA
; APPLICANT:  JAKOBOVITZ, AYA
; TITLE OF INVENTION:  NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION:  USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION:  OTHER CANCERS
; FILE REFERENCE:  51158-20050.00
; CURRENT APPLICATION NUMBER:  US/10/277,292
; CURRENT FILING DATE:  2002-10-21
; PRIOR APPLICATION NUMBER:  US/09/935,430
; PRIOR FILING DATE:  2001-08-22
; PRIOR APPLICATION NUMBER:  60/227,098
; PRIOR FILING DATE:  2000-08-22
; PRIOR APPLICATION NUMBER:  60/282,739

```

; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 451
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-451

Query Match 39.0%; Score 32; DB 14; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLV 9
| |||||
Db 2 PMPKLV 8

RESULT 8

US-10-277-292-555

; Sequence 555, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 555
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-555

Query Match 39.0%; Score 32; DB 14; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLV 9
 | |||||
Db 2 PMPKLV 8

RESULT 9

US-10-280-340-451

; Sequence 451, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 451
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-451

Query Match 39.0%; Score 32; DB 15; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLV 9
 | |||||
Db 2 PMPKLV 8

RESULT 10

US-10-280-340-555

; Sequence 555, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR

```

; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 555
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-555

```

```

Query Match          39.0%; Score 32; DB 15; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches      6; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      3 PFPKLVK 9
        | | | | |
Db      2 PMPKLVK 8

```

RESULT 11

```

US-09-935-430-66
; Sequence 66, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10

```


; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-66

Query Match 39.0%; Score 32; DB 12; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLV 9
| |||||
Db 2 PMPKLV 8

RESULT 12

US-09-935-430-607

; Sequence 607, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 607
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-607

Query Match 39.0%; Score 32; DB 12; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLV 9
| |||||

Db 2 PMPKLKV 8

RESULT 13

US-10-277-292-66

; Sequence 66, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-66

Query Match 39.0%; Score 32; DB 14; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLKV 9
| | | | |
Db 2 PMPKLKV 8

RESULT 14

US-10-277-292-607

; Sequence 607, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA

; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 607
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-607

Query Match 39.0%; Score 32; DB 14; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLV 9
| |||||
Db 2 PMPKLV 8

RESULT 15

US-10-280-340-66

; Sequence 66, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-66

Query Match 39.0%; Score 32; DB 15; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLKV 9
| |||||
Db 2 PMPKLKV 8

RESULT 16

US-10-280-340-607
; Sequence 607, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 607
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-607

Query Match 39.0%; Score 32; DB 15; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLKV 9

Db | |||||
 2 PMPKLKV 8

RESULT 17

US-10-225-567A-1110
; Sequence 1110, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1110
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1110

Query Match 39.0%; Score 32; DB 14; Length 16;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPFPPK 6
 :|||||
Db 8 IKPFPPK 13

RESULT 18

US-09-766-412-39
; Sequence 39, Application US/09766412
; Patent No. US20020103129A1
; GENERAL INFORMATION:
; APPLICANT: GE, Ruowen et al.
; TITLE OF INVENTION: SMALL PEPTIDES HAVING ANTI-ANGIOGENIC AND ENDOTHELIAL
CELL INHIBITION
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 1781-0215P
; CURRENT APPLICATION NUMBER: US/09/766,412
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mammalian
; FEATURE:
; NAME/KEY: misc_feature

; OTHER INFORMATION: shFLT2
US-09-766-412-39

Query Match 37.8%; Score 31; DB 9; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVF 12
| | ||:| |
Db 1 LVPLPKIKNSTF 12

RESULT 19

US-10-226-007-1525
; Sequence 1525, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1525
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Lymphocytic choriomeningitis virus
US-10-226-007-1525

Query Match 37.2%; Score 30.5; DB 14; Length 18;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Qy 3 PFP-KLKVEVFPFP 15
| | |||: | |
Db 1 PLPTKLKISTAPSP 14

RESULT 20

US-09-281-717-31
; Sequence 31, Application US/09281717
; Patent No. US20020061539A1
; GENERAL INFORMATION:
; APPLICANT: Baxter, John D.
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletterick, Robert J.
; APPLICANT: Kushner, Peter J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: West, Brian
; APPLICANT: Yamamoto, Keith R.

```

; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; TITLE OF INVENTION: COACTIVATOR BINDING
; FILE REFERENCE: UCAL-253/02US
; CURRENT APPLICATION NUMBER: US/09/281,717
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 60/079,956
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MUTAGEN
;   LOCATION: (5)
;   OTHER INFORMATION: Leu --> Arg (L454R)
;   FEATURE:
;   NAME/KEY: MUTAGEN
;   LOCATION: (7)
;   OTHER INFORMATION: Leu --> Arg (L456R)
;   FEATURE:
;   NAME/KEY: MUTAGEN
;   LOCATION: (8)
;   OTHER INFORMATION: Glu --> Lys (E457K)
US-09-281-717-31

```

```

Query Match          35.4%; Score 29; DB 9; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches      6; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

```

```

Qy      4 FPKLKVEVF 12
        || | :|||
Db      2 FPPLFLEVF 10

```

```

RESULT 21
US-09-281-717-33
; Sequence 33, Application US/09281717
; Patent No. US20020061539A1
; GENERAL INFORMATION:
; APPLICANT: Baxter, John D.
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletterick, Robert J.
; APPLICANT: Kushner, Peter J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: West, Brian
; APPLICANT: Yamamoto, Keith R.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; TITLE OF INVENTION: COACTIVATOR BINDING
; FILE REFERENCE: UCAL-253/02US
; CURRENT APPLICATION NUMBER: US/09/281,717
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 60/079,956
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 51

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-281-717-33

Query Match 35.4%; Score 29; DB 9; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FPKLKVEVF 12
|| | :|||
Db 2 FPPLFLEVF 10

RESULT 22

US-09-281-717-35

; Sequence 35, Application US/09281717
; Patent No. US20020061539A1
; GENERAL INFORMATION:
; APPLICANT: Baxter, John D.
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletterick, Robert J.
; APPLICANT: Kushner, Peter J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: West, Brian
; APPLICANT: Yamamoto, Keith R.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; TITLE OF INVENTION: COACTIVATOR BINDING
; FILE REFERENCE: UCAL-253/02US
; CURRENT APPLICATION NUMBER: US/09/281,717
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 60/079,956
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-281-717-35

Query Match 35.4%; Score 29; DB 9; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FPKLKVEVF 12
|| | :|||
Db 2 FPPLFLEVF 10

RESULT 23

US-09-935-430-333

; Sequence 333, Application US/09935430
; Publication No. US20030017466A1


```
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 333
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-333
```

```
Query Match          34.1%; Score 28; DB 12; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches      5; Conservative    0; Mismatches    1; Indels      0; Gaps      0;
```

```
Qy          3 PFPKLG 8
              | |||
Db          4 PMPKLG 9
```

RESULT 24

US-10-277-292-333

```
; Sequence 333, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
```

; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 333
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-333

Query Match 34.1%; Score 28; DB 14; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLLK 8
| ||||
Db 4 PMPKLLK 9

RESULT 25
US-10-280-340-333
; Sequence 333, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 333
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-333

Query Match 34.1%; Score 28; DB 15; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLG 8
| | | |
Db 4 PMPKLG 9

RESULT 26

US-09-935-430-269
; Sequence 269, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-269

Query Match 34.1%; Score 28; DB 12; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLG 8
| | | |
Db 5 PMPKLG 10

RESULT 27

US-09-935-430-356
; Sequence 356, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE

```
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 356
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-356
```

```
Query Match          34.1%; Score 28; DB 12; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches      5; Conservative    0; Mismatches    1; Indels      0; Gaps      0;
```

```
QY      3 PFPKLG 8
        | |||
Db      5 PMPKLG 10
```

```
RESULT 28
US-10-033-662-35
; Sequence 35, Application US/10033662
; Publication No. US20030092197A1
; GENERAL INFORMATION:
; APPLICANT: Herman, et al.
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment
of Cardiac
; TITLE OF INVENTION: Response
; FILE REFERENCE: 9195-081
; CURRENT APPLICATION NUMBER: US/10/033,662
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-033-662-35
```

```
Query Match          34.1%; Score 28; DB 14; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.2e+02;
Matches      5; Conservative    1; Mismatches    2; Indels      0; Gaps      0;
```

Qy 8 KVEVFPPF 15
|: | |||
Db 1 KLVVLPFP 8

RESULT 29

US-10-277-292-269

; Sequence 269, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-269

Query Match 34.1%; Score 28; DB 14; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKPK 8
| ||||
Db 5 PMPKPK 10

RESULT 30

US-10-277-292-356

; Sequence 356, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR

```

; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 356
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-356

```

```

Query Match          34.1%; Score 28; DB 14; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches    5; Conservative    0; Mismatches    1; Indels    0; Gaps    0;

```

```

Qy      3 PFPKLK 8
        | |||
Db      5 PMPKLK 10

```

```

RESULT 31
US-10-280-340-269
; Sequence 269, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22

```

; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-269

Query Match 34.1%; Score 28; DB 15; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLK 8
| | | |
Db 5 PMPKLK 10

RESULT 32

US-10-280-340-356
; Sequence 356, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 356
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-356

Query Match 34.1%; Score 28; DB 15; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKLLK 8
| ||||
Db 5 PMPKLLK 10

RESULT 33

US-09-918-171A-29
; Sequence 29, Application US/09918171A
; Patent No. US20020110894A1
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/04193
; CURRENT APPLICATION NUMBER: US/09/918,171A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/369,364
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-918-171A-29

Query Match 34.1%; Score 28; DB 9; Length 14;
Best Local Similarity 62.5%; Pred. No. 8.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKPFKLLK 8
: || |||:
Db 6 IKPKPKLLQ 13

RESULT 34

US-09-947-124-5
; Sequence 5, Application US/09947124
; Patent No. US20020064849A1
; GENERAL INFORMATION:
; APPLICANT: Herr, John
; APPLICANT: Visconti, Pablo
; APPLICANT: Mandal, Arabinda
; APPLICANT: Khole, Vrinda
; TITLE OF INVENTION: Human Soluble Testicular Adenylyl Cyclase
; FILE REFERENCE: 00582-03
; CURRENT APPLICATION NUMBER: US/09/947,124
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,207
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 16

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-947-124-5

Query Match 34.1%; Score 28; DB 9; Length 16;
Best Local Similarity 45.5%; Pred. No. 1e+03;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEV 11
||| |:|:: :
Db 3 LKPDPELEMSL 13

RESULT 35
US-10-203-334-2
; Sequence 2, Application US/10203334
; Publication No. US20040038417A1
; GENERAL INFORMATION:
; APPLICANT: Max-Planck-Gesellschaft zur Forderung der Wissenschaften e.V.
; APPLICANT: CAHILL, DOLORES, J.
; APPLICANT: NORDHOFF, ECKHARD
; APPLICANT: KLOSE, JOACHIM
; APPLICANT: EICKHOFF, HOLGER
; APPLICANT: SCHMIDT, FRANK
; APPLICANT: LEHRACH, HANS
; TITLE OF INVENTION: Method for identifying and/or characterizing a
(poly)peptide
; FILE REFERENCE: 009848-0272307
; CURRENT APPLICATION NUMBER: US/10/203,334
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/EP01/01332
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: EP 00 10 2567.5
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-203-334-2

Query Match 32.9%; Score 27; DB 12; Length 10;
Best Local Similarity 55.6%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LKVEVFPFP 15
| | : |||
Db 1 LAVNMVPFP 9

RESULT 36
US-10-601-837-131
; Sequence 131, Application US/10601837
; Publication No. US20040053309A1
; GENERAL INFORMATION:
; APPLICANT: Holt, Gordon D

```
; APPLICANT: Kelly, Michael D
; APPLICANT: Kennedy, Sandra J
; APPLICANT: Moyses, Christopher
; TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment
of Kidney
; TITLE OF INVENTION: Response
; FILE REFERENCE: 2543-1-030
; CURRENT APPLICATION NUMBER: US/10/601,837
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: PCT/GB01/05777
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: US 60/260392
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Ratus No. US20040053309Alvegicus
US-10-601-837-131
```

```
Query Match          32.9%; Score 27; DB 12; Length 10;
Best Local Similarity 55.6%; Pred. No. 8.9e+02;
Matches      5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      7 LKVEVFPPF 15
        | | : |||
Db      1 LAVNMVPPF 9
```

RESULT 37

US-09-988-493-133

```
; Sequence 133, Application US/09988493
; Publication No. US20030064419A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: O'Hare, Michael John
; APPLICANT: Page, Martin John
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Waterfield, Michael Derek
; TITLE OF INVENTION: Proteins, Genes, and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer
; FILE REFERENCE: 2543-1-024
; CURRENT APPLICATION NUMBER: US/09/988,493
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: PCT/GB01/01219
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: GB 0006695.1
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: GB 0007265.2
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapien
```

US-09-988-493-133

Query Match 32.9%; Score 27; DB 12; Length 10;
Best Local Similarity 55.6%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LKVEVFPPF 15
| | : |||
Db 1 LAVNMVPPF 9

RESULT 38

US-10-014-340-427

; Sequence 427, Application US/10014340

; Publication No. US20030064411A1

; GENERAL INFORMATION:

; APPLICANT: Herath, et al

; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor,
Including

; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease

; FILE REFERENCE: 9195-078

; CURRENT APPLICATION NUMBER: US/10/014,340

; CURRENT FILING DATE: 2001-12-10

; NUMBER OF SEQ ID NOS: 823

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 427

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-014-340-427

Query Match 32.9%; Score 27; DB 12; Length 10;
Best Local Similarity 55.6%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LKVEVFPPF 15
| | : |||
Db 1 LAVNMVPPF 9

RESULT 39

US-10-014-340-428

; Sequence 428, Application US/10014340

; Publication No. US20030064411A1

; GENERAL INFORMATION:

; APPLICANT: Herath, et al

; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor,
Including

; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease

; FILE REFERENCE: 9195-078

; CURRENT APPLICATION NUMBER: US/10/014,340

; CURRENT FILING DATE: 2001-12-10

; NUMBER OF SEQ ID NOS: 823

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 428

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-014-340-428

Query Match 32.9%; Score 27; DB 12; Length 10;
Best Local Similarity 55.6%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LKVEVFPFP 15
| | : |||
Db 1 LAVNMVFPF 9

RESULT 40

US-10-100-049-25

; Sequence 25, Application US/10100049

; Publication No. US20030078398A1

; GENERAL INFORMATION:

; APPLICANT: Graham, Margaret

; APPLICANT: Smith, Trevor

; APPLICANT: Munn, Edward

; APPLICANT: Knox, David

; APPLICANT: Oliver, Joanna

; APPLICANT: Newton, Susan

; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING AMINOPEPTIDASE ENZYMES

; TITLE OF INVENTION: AND THEIR USE IN THE PREPARATION OF VACCINES AGAINST
HELMINTH

; TITLE OF INVENTION: INFECTIONS

; FILE REFERENCE: 1181-261

; CURRENT APPLICATION NUMBER: US/10/100,049

; CURRENT FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: US 09/129366

; PRIOR FILING DATE: 1998-08-05

; PRIOR APPLICATION NUMBER: US 08/335844

; PRIOR FILING DATE: 1995-01-09

; PRIOR APPLICATION NUMBER: PCT/GB93/00943

; PRIOR FILING DATE: 1993-05-07

; PRIOR APPLICATION NUMBER: GB 9209993.6

; PRIOR FILING DATE: 1992-05-08

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 25

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Haemonchus contortus

US-10-100-049-25

Query Match 32.9%; Score 27; DB 14; Length 11;
Best Local Similarity 55.6%; Pred. No. 9.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FPKLKVEVF 12
: | : ||| |
Db 3 YPVVKVEEF 11

RESULT 41

US-10-340-458-24

; Sequence 24, Application US/10340458
; Publication No. US20030175920A1
; GENERAL INFORMATION:
; APPLICANT: Bonny, Christophe
; TITLE OF INVENTION: Cell-permeable peptide inhibitors of the JNK signal
; TITLE OF INVENTION: transduction pathway
; FILE REFERENCE: 20349-501B
; CURRENT APPLICATION NUMBER: US/10/340,458
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/347,062
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically synthesized
US-10-340-458-24

Query Match 32.9%; Score 27; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KPFPKLVKEV 11
:| ||: ||
Db 2 RPSPKMGVSV 11

RESULT 42
US-10-308-128-144
; Sequence 144, Application US/10308128
; Publication No. US20040033506A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN MITOCHONDRIAL AND
MICROSOMAL
; TITLE OF INVENTION: GLYCEROL-3-PHOSPHATE ACYLTRANSFERASES AND VARIANTS
THEREOF
; FILE REFERENCE: D0199 NP
; CURRENT APPLICATION NUMBER: US/10/308,128
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: U.S. 60/334,904
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 144
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-308-128-144

Query Match 32.9%; Score 27; DB 12; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 FPKLKVEVFP 13
| |::|| |
Db 5 FTKVEVEFMP 14

RESULT 43

US-10-226-007-1513
; Sequence 1513, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1513
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Lymphocytic choriomeningitis virus
US-10-226-007-1513

Query Match 32.9%; Score 27; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 KLKVEVFPFP 15
|||: | |
Db 1 KLIKISTAPSP 10

RESULT 44

US-09-774-639-257
; Sequence 257, Application US/09774639
; Publication No. US20030003555A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-257

Query Match 32.9%; Score 27; DB 10; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KVEVFPPF 15
:::|| ||
Db 2 RLQVFSFP 9

RESULT 45

US-09-969-730-339

; Sequence 339, Application US/09969730

; Publication No. US20030054443A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: 90 Human Secreted Proteins

; FILE REFERENCE: PZ013P2

; CURRENT APPLICATION NUMBER: US/09/969,730

; CURRENT FILING DATE: 2001-10-04

; PRIOR APPLICATION NUMBER: 09/774,639

; PRIOR FILING DATE: 2001-02-01

; PRIOR APPLICATION NUMBER: 60/238,291

; PRIOR FILING DATE: 2000-10-06

; PRIOR APPLICATION NUMBER: 09/244,112

; PRIOR FILING DATE: 1999-02-04

; PRIOR APPLICATION NUMBER: PCT/US98/16235

; PRIOR FILING DATE: 1998-08-04

; PRIOR APPLICATION NUMBER: 60/056,371

; PRIOR FILING DATE: 1997-08-19

; PRIOR APPLICATION NUMBER: 60/056,732

; PRIOR FILING DATE: 1997-08-19

; PRIOR APPLICATION NUMBER: 60/056,366

; PRIOR FILING DATE: 1997-08-19

; PRIOR APPLICATION NUMBER: 60/056,364

; PRIOR FILING DATE: 1997-08-19

; PRIOR APPLICATION NUMBER: 60/056,370

; PRIOR FILING DATE: 1997-08-19

; PRIOR APPLICATION NUMBER: 60/056,367

; PRIOR FILING DATE: 1997-08-19

; PRIOR APPLICATION NUMBER: 60/056,365

; PRIOR FILING DATE: 1997-08-19

; PRIOR APPLICATION NUMBER: 60/056,731

; PRIOR FILING DATE: 1997-08-19

; PRIOR APPLICATION NUMBER: 60/056,557

; PRIOR FILING DATE: 1997-08-19

; PRIOR APPLICATION NUMBER: 60/056,563

; PRIOR FILING DATE: 1997-08-19

; PRIOR APPLICATION NUMBER: 60/055,970

; PRIOR FILING DATE: 1997-08-18

; PRIOR APPLICATION NUMBER: 60/055,986

; PRIOR FILING DATE: 1997-08-18

; PRIOR APPLICATION NUMBER: 60/055,311

; PRIOR FILING DATE: 1997-08-05

; PRIOR APPLICATION NUMBER: 60/054,808

; PRIOR FILING DATE: 1997-08-05

; PRIOR APPLICATION NUMBER: 60/054,803

; PRIOR FILING DATE: 1997-08-05

```

; PRIOR APPLICATION NUMBER: 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,809
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,806
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,310
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,798
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,309
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,312
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,807
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,386
; PRIOR FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 339
; LENGTH: 15
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-969-730-339

```

```

Query Match          32.9%; Score 27; DB 10; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches      4; Conservative      3; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      8 KVEVFPFP 15
        :::|| ||
Db      2 RLQVFSFP 9

```

RESULT 46

```

US-10-682-420-80
; Sequence 80, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08

```


; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-682-420-80

Query Match 32.9%; Score 27; DB 12; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KLKVEVFP 13
|:| | :|
Db 8 KVKVEFWP 15

RESULT 47

US-10-682-420-81
; Sequence 81, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 81
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-682-420-81

Query Match 32.9%; Score 27; DB 12; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KLKVEVFP 13
|:|:|:|
Db 4 KVKVEFWP 11

RESULT 48

US-10-226-007-1514

; Sequence 1514, Application US/10226007

; Publication No. US20030105277A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

; FILE REFERENCE: 5005.01

; CURRENT APPLICATION NUMBER: US/10/226,007

; CURRENT FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: US 60/313,883

; PRIOR FILING DATE: 2001-08-21

; NUMBER OF SEQ ID NOS: 1673

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1514

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Lymphocytic choriomeningitis virus

US-10-226-007-1514

Query Match 32.9%; Score 27; DB 14; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 KLKVEVFPFP 15
|:|:|:|
Db 1 KLIKISTAPSP 10

RESULT 49

US-10-226-007-1516

; Sequence 1516, Application US/10226007

; Publication No. US20030105277A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

; FILE REFERENCE: 5005.01

; CURRENT APPLICATION NUMBER: US/10/226,007

; CURRENT FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: US 60/313,883

; PRIOR FILING DATE: 2001-08-21

; NUMBER OF SEQ ID NOS: 1673

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1516

; LENGTH: 15
; TYPE: PRT
; ORGANISM: Lymphocytic choriomeningitis virus
US-10-226-007-1516

Query Match 32.9%; Score 27; DB 14; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 KLKVEVFPFP 15
|||: ||
Db 2 KLIKISTAPSP 11

RESULT 50

US-10-621-363-339

; Sequence 339, Application US/10621363
; Publication No. US20040023283A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P2C1
; CURRENT APPLICATION NUMBER: US/10/621,363
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 339
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-621-363-339

Query Match 32.9%; Score 27; DB 16; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KVEVFPP 15
 ::|| ||
Db 2 RLQVFSFP 9

Search completed: July 4, 2004, 05:12:31
Job time : 31.4403 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:51 ; Search time 25.5224 Seconds
(without alignments)
185.436 Million cell updates/sec

Title: US-09-641-802-8
Perfect score: 82
Sequence: 1 LKPFPKLKVEVFPPF 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 5664

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query
No. Score Match Length DB ID Description

1	30	36.6	14	10	P82435	P82435 nicotiana t
2	29	35.4	15	10	Q9S929	Q9s929 glycine max
3	29	35.4	16	6	Q9BGG8	Q9bgg8 sorex arane
4	26	31.7	18	11	Q9QVI1	Q9qvil rattus sp.
5	25	30.5	17	11	Q9JLA7	Q9jla7 mus musculu
6	24	29.3	16	2	Q9R4J0	Q9r4j0 arthrobacte
7	24	29.3	17	8	Q9T5Z9	Q9t5z9 pimelodella
8	23	28.0	11	5	P82700	P82700 leucophaea
9	23	28.0	17	6	Q9TRH5	Q9trh5 bos taurus
10	23	28.0	18	3	Q06711	Q06711 saccharomyc
11	22	26.8	11	11	Q9QYF6	Q9qyf6 mus musculu
12	22	26.8	16	8	Q8MC25	Q8mc25 sonneratia
13	22	26.8	16	8	Q8MC39	Q8mc39 ammannia ba
14	22	26.8	16	8	Q8LVE1	Q8lve1 punica gran
15	22	26.8	16	8	Q8MC53	Q8mc53 woodfordia
16	22	26.8	16	8	Q8MC17	Q8mc17 ludwigia hy
17	22	26.8	16	8	Q8LVE2	Q8lve2 lythrum sal
18	22	26.8	16	8	Q8LVE0	Q8lve0 trapa maxim
19	22	26.8	16	8	Q8MET2	Q8met2 saxifraga s
20	22	26.8	16	8	Q8MC45	Q8mc45 decodon ver
21	22	26.8	16	8	Q8MC21	Q8mc21 combretum w
22	22	26.8	16	8	Q8MC51	Q8mc51 cuphea lanc
23	22	26.8	16	8	Q8MC33	Q8mc33 rotala indi
24	22	26.8	16	8	Q8MC19	Q8mc19 quisqualis
25	22	26.8	16	8	Q8MC49	Q8mc49 pemphis aci
26	22	26.8	16	8	Q8MC27	Q8mc27 lagerstroem
27	22	26.8	16	8	Q8MET0	Q8met0 cercidiphyl
28	22	26.8	16	8	Q8MC23	Q8mc23 sonneratia
29	22	26.8	16	8	Q8MC41	Q8mc41 nesaea lued
30	22	26.8	16	8	Q8MC15	Q8mc15 fuchsia hyb
31	22	26.8	16	8	Q8MC43	Q8mc43 sonneratia
32	22	26.8	16	8	Q8MC47	Q8mc47 peplis port
33	22	26.8	16	8	Q8MC37	Q8mc37 lawsonia in
34	22	26.8	16	8	Q8MC29	Q8mc29 duabanga gr
35	22	26.8	16	8	Q8MC31	Q8mc31 lagerstroem
36	22	26.8	16	8	Q8MES8	Q8mes8 daphniphyll
37	22	26.8	16	8	Q8MC35	Q8mc35 heimia myrt
38	22	26.8	16	10	Q94F61	Q94f61 triticum ae
39	22	26.8	17	8	Q9XQN9	Q9xqn9 sinapis alb
40	22	26.8	17	16	Q8X4A4	Q8x4a4 escherichia
41	21	25.6	13	2	Q9R8R9	Q9r8r9 streptococc
42	21	25.6	14	4	P78359	P78359 homo sapien
43	21	25.6	15	4	Q9HCX8	Q9hcx8 homo sapien
44	21	25.6	16	2	Q44610	Q44610 buchnera ap
45	21	25.6	16	4	Q9UD41	Q9ud41 homo sapien
46	21	25.6	17	4	Q9UC23	Q9uc23 homo sapien
47	20	24.4	10	13	Q9PS07	Q9ps07 alligator m
48	20	24.4	12	8	Q36668	Q36668 pinus sylve
49	20	24.4	12	8	Q37791	Q37791 larix eurol
50	20	24.4	14	2	Q52636	Q52636 escherichia
51	20	24.4	15	2	Q52304	Q52304 escherichia
52	20	24.4	16	6	Q9TQZ7	Q9tqz7 bos taurus
53	20	24.4	17	1	Q50842	Q50842 methanococc
54	20	24.4	17	6	Q29395	Q29395 canis famil
55	20	24.4	17	15	Q9EL24	Q9el24 human immun
56	20	24.4	18	4	Q96C65	Q96c65 homo sapien
57	20	24.4	18	8	O98365	O98365 myosurus mi

58	20	24.4	18	11	P70649	P70649 mus sp. syn
59	20	24.4	18	11	P70650	P70650 mus sp. syn
60	20	24.4	18	11	Q7TQB5	Q7tqb5 mus musculu
61	20	24.4	18	17	Q9UYK7	Q9uyk7 pyrococcus
62	19.5	23.8	14	11	Q99PB8	Q99pb8 mus musculu
63	19.5	23.8	17	4	Q9UCS0	Q9ucs0 homo sapien
64	19	23.2	8	10	Q8GTG5	Q8gtg5 lycopersico
65	19	23.2	11	5	Q95PX6	Q95px6 caenorhabdi
66	19	23.2	11	11	P97755	P97755 rattus norv
67	19	23.2	12	2	Q8KZ86	Q8kz86 acinetobact
68	19	23.2	12	8	Q9GI96	Q9gi96 sargassum p
69	19	23.2	12	8	O03816	O03816 metasequoia
70	19	23.2	12	8	O03815	O03815 abies alba
71	19	23.2	12	8	Q36669	Q36669 pinus sylve
72	19	23.2	12	8	Q37790	Q37790 larix eurol
73	19	23.2	13	8	P92460	P92460 taxus bacca
74	19	23.2	13	8	Q36622	Q36622 picea abies
75	19	23.2	14	4	Q9P2A2	Q9p2a2 homo sapien
76	19	23.2	14	5	Q10757	Q10757 theromyzon
77	19	23.2	14	11	Q9JJU5	Q9jju5 mus musculu
78	19	23.2	14	11	Q8CFB6	Q8cfb6 mus musculu
79	19	23.2	15	2	Q9KIV5	Q9kiv5 anabaena sp
80	19	23.2	15	4	Q9UCH4	Q9uch4 homo sapien
81	19	23.2	16	2	Q9F9S4	Q9f9s4 helicobacte
82	19	23.2	16	6	Q9TQY6	Q9tqy6 oryctolagus
83	19	23.2	16	9	Q38407	Q38407 bacterioph
84	19	23.2	16	11	Q9ERP8	Q9erp8 rattus norv
85	19	23.2	17	2	Q9ETL3	Q9etl3 helicobacte
86	19	23.2	17	2	Q9LB06	Q9lb06 prochloroco
87	19	23.2	17	4	Q96P96	Q96p96 homo sapien
88	19	23.2	17	4	Q9UCC6	Q9ucc6 homo sapien
89	19	23.2	17	5	Q9TWR3	Q9twr3 trypanosoma
90	19	23.2	17	6	Q9TR21	Q9tr21 sus scrofa
91	19	23.2	18	4	Q9UCY8	Q9ucy8 homo sapien
92	19	23.2	18	5	Q965L9	Q965l9 caenorhabdi
93	19	23.2	18	6	Q9TT81	Q9tt81 bos taurus
94	19	23.2	18	11	Q9WTP8	Q9wtp8 rattus norv
95	18.5	22.6	18	4	Q9H1I3	Q9hli3 homo sapien
96	18	22.0	8	4	Q9UJ50	Q9uj50 homo sapien
97	18	22.0	9	6	Q28121	Q28121 bos taurus
98	18	22.0	9	6	Q9TRU7	Q9tru7 bos taurus
99	18	22.0	9	10	Q9S8J8	Q9s8j8 oryza sativ
100	18	22.0	10	4	Q9UDE8	Q9ude8 homo sapien

ALIGNMENTS

RESULT 1

P82435

ID P82435 PRELIMINARY; PRT; 14 AA.

AC P82435;

DT 01-JUN-2000 (TrEMBLrel. 14, Created)

DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE 29 kDa cell wall protein (Fragment).

OS Nicotiana tabacum (Common tobacco).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture.";
 RL Planta 0:0-0(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 DR GO; GO:0005618; C:cell wall; IEA.
 KW Cell wall.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1645 MW; CA0D490EF7F851B2 CRC64;

Query Match 36.6%; Score 30; DB 10; Length 14;
 Best Local Similarity 45.5%; Pred. No. 2.8e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 FPKLKVEVFPF 14
 :|: |:|| |
 Db 2 YPRKTVDVFTF 12

RESULT 2

Q9S929

ID Q9S929 PRELIMINARY; PRT; 15 AA.
 AC Q9S929;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Pyrroline-5-carboxylate reductase, P5CR (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91378472; PubMed=1898034;
 RA Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;
 RT "Pyrroline-5-carboxylate reductase in soybean nodules:
 RT isolation/partial primary structure/evidence for isozymes.";
 RL Arch. Biochem. Biophys. 288:350-357(1991).
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1715 MW; D9821F773F3DF524 CRC64;

Query Match 35.4%; Score 29; DB 10; Length 15;
 Best Local Similarity 57.1%; Pred. No. 4.4e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEVPFPF 15
 :|:|| |

Db 1 MEIFPIP 7

RESULT 3

Q9BGG8

ID Q9BGG8 PRELIMINARY; PRT; 16 AA.
AC Q9BGG8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Thyroid hormone receptor alpha (Fragment).
GN THRA1.
OS Sorex araneus (Eurasian common shrew) (European shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.
OX NCBI_TaxID=42254;
RN [1]
RP SEQUENCE FROM N.A.
RA Larkin D., Serov O., Zhdanova N.;
RT "Mapping of five genes from human chromosome 17 to chromosome hn of
RT the common shrew (Sorex araneus).";
RL Acta Theriol. (Warsz) 45:143-146(2000).
DR EMBL; AF314827; AAK13419.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1951 MW; 775186E3FE5F52E2 CRC64;

Query Match 35.4%; Score 29; DB 6; Length 16;
Best Local Similarity 66.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FPKLKVEVF 12
|| | :|||
Db 3 FPPLFLEVF 11

RESULT 4

Q9QVII

ID Q9QVII PRELIMINARY; PRT; 18 AA.
AC Q9QVII;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Sucrase-alpha-dextrinase subunit beta, S-D subunit beta
DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92031479; PubMed=1931964;
RA Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.;
RT "Structural and functional correlates of sucrase-alpha-dextrinase in
RT intact brush border membranes.";
RL Biochemistry 30:10399-10408(1991).

FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2122 MW; 68FF1ABA87B24E49 CRC64;

Query Match 31.7%; Score 26; DB 11; Length 18;
Best Local Similarity 55.6%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLV 11
| :|:|
Db 7 PISELRV 15

RESULT 5

Q9JLA7

ID Q9JLA7 PRELIMINARY; PRT; 17 AA.
AC Q9JLA7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Fibroblast growth factor homologous factor 3 isoform 1B
DE (Fragment).
GN FHF-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112823; PubMed=10644718;
RA Munoz-Sanjuan I., Smallwood P.M., Nathans J.;
RT "Isoform Diversity among Fibroblast Growth Factor Homologous Factors
RT Is Generated by Alternative Promoter Usage and Differential
RT Splicing.";
RL J. Biol. Chem. 275:2589-2597(2000).
DR EMBL; AF199604; AAF31391.1; -.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1870 MW; 9A0E0364E696D949 CRC64;

Query Match 30.5%; Score 25; DB 11; Length 17;
Best Local Similarity 62.5%; Pred. No. 2.4e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKPFKLV 8
| | |:
Db 3 LSPEQLK 10

RESULT 6

Q9R4J0

ID Q9R4J0 PRELIMINARY; PRT; 16 AA.
AC Q9R4J0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE LIMONATE dehydrogenase (Fragment).
OS Arthrobacter globiformis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcineae; Micrococcaceae; Arthrobacter.
 OX NCBI_TaxID=1665;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96045380; PubMed=7546548;
 RA Suhayda C.G., Omura M., Hasegawa S.;
 RT "Limonoate dehydrogenase from Arthrobacter globiformis: the native
 RT enzyme and its N-terminal sequence."
 RL Phytochemistry 40:17-20(1995).
 SQ SEQUENCE 16 AA; 1759 MW; 514B2DE906FD5984 CRC64;

Query Match 29.3%; Score 24; DB 2; Length 16;
 Best Local Similarity 55.6%; Pred. No. 3.3e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
 || :|: ||
 Db 2 PFNRLENEV 10

RESULT 7

Q9T5Z9

ID Q9T5Z9 PRELIMINARY; PRT; 17 AA.
 AC Q9T5Z9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE ATPase subunit 8 (Fragment).
 GN ATPASE8.
 OS Pimelodella chagresi.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Pimelodidae; Pimelodella.
 OX NCBI_TaxID=71257;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98291472; PubMed=9628002;
 RA Bermingham E., Martin A.P.;
 RT "Comparative mtDNA phylogeography of neotropical freshwater fishes:
 RT testing shared history to infer the evolutionary landscape of lower
 RT Central America."
 RL Mol. Ecol. 7:499-517(1998).
 DR EMBL; AF040423; AAC77594.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1 1
 SQ SEQUENCE 17 AA; 2113 MW; 40325E578612222A CRC64;

Query Match 29.3%; Score 24; DB 8; Length 17;
 Best Local Similarity 50.0%; Pred. No. 3.5e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 KLKVEVFPFP 15
 ||| | : :|
 Db 6 KLKSETWNWP 15

RESULT 8

P82700

ID P82700 PRELIMINARY; PRT; 11 AA.
 AC P82700;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Periviscerokinin-3 (LEM-PVK-3).
 OS Leucophaea maderae (Madeira cockroach),
 OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
 OS Blaberus craniifer,
 OS Blaptica dubia (Argentinian wood cockroach), and
 OS Gromphadorina portentosa (Cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
 RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
 RX MEDLINE=20307624; PubMed=10849006;
 RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
 RT "Identification of novel periviscerokinins from single neurohaemal
 RT release sites in insects. MS/MS fragmentation complemented by Edman
 RT degradation.";
 RL Eur. J. Biochem. 267:3869-3873(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -!- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;

Query Match 28.0%; Score 23; DB 5; Length 11;
 Best Local Similarity 60.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFPKL 7
 |||::
 Db 7 PFPRV 11

RESULT 9

Q9TRH5

ID Q9TRH5 PRELIMINARY; PRT; 17 AA.
 AC Q9TRH5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Alpha-S1-casein homolog (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=93231344; PubMed=1299613;
RA Neuteboom B., Giuffrida M.G., Conti A.;
RT "Isolation of a new ligand-carrying casein fragment from bovine
RT mammary gland microsomes.";
RL FEBS Lett. 305:189-191(1992).
SQ SEQUENCE 17 AA; 1950 MW; 8890EF0685A0537F CRC64;

Query Match 28.0%; Score 23; DB 6; Length 17;
Best Local Similarity 60.0%; Pred. No. 5.2e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 3 PFPKLKVEVF 12
||| |||
Db 4 PFP----EVF 9

RESULT 10

Q06711

ID Q06711 PRELIMINARY; PRT; 18 AA.
AC Q06711;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Ubiquitin (Fragment).
GN UBI1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YPH1;
RX MEDLINE=94024010; PubMed=8211183;
RA Ota I.M., Varshavsky A.;
RT "A yeast protein similar to bacterial two-component regulators.";
RL Science 262:566-569(1993).
DR EMBL; U01835; AAC48913.1; -.
SQ SEQUENCE 18 AA; 2249 MW; D13E4F7C1DBBFDD1 CRC64;

Query Match 28.0%; Score 23; DB 3; Length 18;
Best Local Similarity 62.5%; Pred. No. 5.5e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKPFPPKLK 8
|:| |||
Db 11 LRPKKKLK 18

RESULT 11

Q9QYF6

ID Q9QYF6 PRELIMINARY; PRT; 11 AA.
AC Q9QYF6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Pancreas transcription factor1 p48 subunit (Fragment).
 GN PTF1P48.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129sv;
 RA Obata J., Mimura H., Goto T., Nakayama R., Kondo M., Oka C.,
 RA Kawaichi M.;
 RT "p48 subunit of mouse PTF1 binds to RBP-Jkappa/CBF-1, the
 RT intracellular mediator of Notch signaling, and is expressed in the
 RT neural tube of the early stage embryos."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB035674; BAA88247.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1327 MW; CA4662F8E3372732 CRC64;

Query Match 26.8%; Score 22; DB 11; Length 11;
 Best Local Similarity 66.7%; Pred. No. 5e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKPFPPK 6
 || ||:
 Db 6 LKHFFPR 11

RESULT 12
 Q8MC25

ID Q8MC25 PRELIMINARY; PRT; 16 AA.
 AC Q8MC25;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PsA (Fragment).
 GN PSAA.
 OS Sonneratia apetala.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Sonneratia.
 OX NCBI_TaxID=122813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S165;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences."
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035740; AAL14161.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
| |::|: |
Db 6 PEPEVKILV 14

RESULT 13

Q8MC39

ID Q8MC39 PRELIMINARY; PRT; 16 AA.
AC Q8MC39;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Ammannia baccifera.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Ammannia.
OX NCBI_TaxID=162022;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A610;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences."
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035733; AAL14147.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
| |::|: |
Db 6 PEPEVKILV 14

RESULT 14

Q8LVE1

ID Q8LVE1 PRELIMINARY; PRT; 16 AA.
AC Q8LVE1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN PSAA.

```

OS   Punica granatum (Pomegranate).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   Myrtales; Lythraceae; Punica.
OX   NCBI_TaxID=22663;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=P728, and P745;
RA   Huang Y., Shi S.;
RT   "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT   on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT   Transcribed Spacer (ITS) Sequences.";
RL   Int. J. Plant Sci. 163:215-225(2002).
DR   EMBL; AY035724; AAL14129.1; -.
DR   EMBL; AY035742; AAL14165.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER      16      16
SQ   SEQUENCE     16 AA;  1895 MW;  517FE691B89355B9 CRC64;

Query Match          26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches      4; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

Qy      3 PFPKLVKEV 11
      | |::|: |
Db      6 PEPEVKILV 14

```

RESULT 15

Q8MC53

```

ID   Q8MC53          PRELIMINARY;          PRT;          16 AA.
AC   Q8MC53;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   PsaA (Fragment).
GN   PSAA.
OS   Woodfordia fruticosa.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   Myrtales; Lythraceae; Woodfordia.
OX   NCBI_TaxID=141189;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=W493;
RA   Huang Y., Shi S.;
RT   "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT   on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT   Transcribed Spacer (ITS) Sequences.";
RL   Int. J. Plant Sci. 163:215-225(2002).
DR   EMBL; AY035722; AAL14125.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER      16      16

```


SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
| |::|: |
Db 6 PEPEVKILV 14

RESULT 16

Q8MC17

ID Q8MC17 PRELIMINARY; PRT; 16 AA.
AC Q8MC17;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Ludwigia hyssopifolia.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Onagraceae; Ludwigia.
OX NCBI_TaxID=155013;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L787;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences."
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035745; AAL14171.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
| |::|: |
Db 6 PEPEVKILV 14

RESULT 17

Q8LVE2

ID Q8LVE2 PRELIMINARY; PRT; 16 AA.
AC Q8LVE2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsaA (Fragment).

GN PSAA.
 OS *Lythrum salicaria* (Purple loosestrife).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Lythrum.
 OX NCBI_TaxID=13129;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L758, and 758F;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035727; AAL14135.1; -.
 DR EMBL; AF421495; AAM45853.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
 Best Local Similarity 44.4%; Pred. No. 7.2e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
 | |::|:|
 Db 6 PEPEVKILV 14

RESULT 18

Q8LVE0

ID Q8LVE0 PRELIMINARY; PRT; 16 AA.
 AC Q8LVE0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PsaA (Fragment).
 GN PSAA.
 OS *Trapa maximowiczii*.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Trapa.
 OX NCBI_TaxID=162053;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=T744, and T010;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035729; AAL14139.1; -.
 DR EMBL; AY035730; AAL14141.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
| |::|: |
Db 6 PEPEVKILV 14

RESULT 19

Q8MET2

ID Q8MET2 PRELIMINARY; PRT; 16 AA.
AC Q8MET2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PSI P700 apoprotein A1 (Fragment).
GN PSAA.
OS Saxifraga stolonifera.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Saxifragaceae; Saxifraga.
OX NCBI_TaxID=182070;
RN [1]
RP SEQUENCE FROM N.A.
RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;
RT "Phylogeny of the Altingiaceae based on cpDNA matK, PY-IGS and nrDNA
RT ITS sequences.";
RL Plant Syst. Evol. 230:13-24(2001).
DR EMBL; AF377995; AAM45512.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
| |::|: |
Db 6 PEPEVKILV 14

RESULT 20

Q8MC45

ID Q8MC45 PRELIMINARY; PRT; 16 AA.
AC Q8MC45;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsaA (Fragment).

GN PSAA.
 OS Decodon verticillatus (Swamp loosestrife).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Decodon.
 OX NCBI_TaxID=162018;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D212;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences."
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035728; AAL14137.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

 Query Match 26.8%; Score 22; DB 8; Length 16;
 Best Local Similarity 44.4%; Pred. No. 7.2e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

 Qy 3 PFPKLKVEV 11
 | |::|: |
 Db 6 PEPEVKILV 14

RESULT 21

Q8MC21
 ID Q8MC21 PRELIMINARY; PRT; 16 AA.
 AC Q8MC21;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PsaA (Fragment).
 GN PSAA.
 OS Combretum wallichii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Combretaceae; Combretum.
 OX NCBI_TaxID=131243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C505;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences."
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035743; AAL14167.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16 16

SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11

| |::|: |

Db 6 PEPEVKILV 14

RESULT 22

Q8MC51

ID Q8MC51 PRELIMINARY; PRT; 16 AA.

AC Q8MC51;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE PsaA (Fragment).

GN PSAA.

OS Cuphea lanceolata.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC Myrtales; Lythraceae; Cuphea.

OX NCBI_TaxID=3930;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C490;

RA Huang Y., Shi S.;

RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based

RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal

RT Transcribed Spacer (ITS) Sequences.";

RL Int. J. Plant Sci. 163:215-225(2002).

DR EMBL; AY035723; AAL14127.1; -.

DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

FT NON_TER 16 16

SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11

| |::|: |

Db 6 PEPEVKILV 14

RESULT 23

Q8MC33

ID Q8MC33 PRELIMINARY; PRT; 16 AA.

AC Q8MC33;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE PsaA (Fragment).

GN PSAA.
 OS Rotala indica.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Rotala.
 OX NCBI_TaxID=162024;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R492;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035736; AAL14153.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

 Query Match 26.8%; Score 22; DB 8; Length 16;
 Best Local Similarity 44.4%; Pred. No. 7.2e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

 Qy 3 PFPKLVKEV 11
 | |::|: |
 Db 6 PEPEVKILV 14

RESULT 24

Q8MC19

ID Q8MC19 PRELIMINARY; PRT; 16 AA.
 AC Q8MC19;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PsaA (Fragment).
 GN PSAA.
 OS Quisqualis indica (Rangoon creeper).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Combretaceae; Quisqualis.
 OX NCBI_TaxID=3956;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Q379;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035744; AAL14169.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16 16

SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11

| |::|: |

Db 6 PEPEVKILV 14

RESULT 25

Q8MC49

ID Q8MC49 PRELIMINARY; PRT; 16 AA.

AC Q8MC49;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE PsaA (Fragment).

GN PSAA.

OS Pemphigus acidula.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC Myrtales; Lythraceae; Pemphigus.

OX NCBI_TaxID=126635;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=P630;

RA Huang Y., Shi S.;

RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based

RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal

RT Transcribed Spacer (ITS) Sequences.";

RL Int. J. Plant Sci. 163:215-225(2002).

DR EMBL; AY035725; AAL14131.1; -.

DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

FT NON_TER 16 16

SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11

| |::|: |

Db 6 PEPEVKILV 14

RESULT 26

Q8MC27

ID Q8MC27 PRELIMINARY; PRT; 16 AA.

AC Q8MC27;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE PsaA (Fragment).

GN PSAA.
 OS Lagerstroemia villosa.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Lagerstroemia.
 OX NCBI_TaxID=162025;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L688;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035739; AAL14159.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
 Best Local Similarity 44.4%; Pred. No. 7.2e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLKVEV 11
 | |::|: |
 Db 6 PEPEVKILV 14

RESULT 27

Q8MET0

ID Q8MET0 PRELIMINARY; PRT; 16 AA.
 AC Q8MET0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PSI P700 apoprotein A1 (Fragment).
 GN PSAA.
 OS Cercidiphyllum japonicum (Katsura tree).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Saxifragales; Cercidiphyllaceae; Cercidiphyllum.
 OX NCBI_TaxID=13413;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;
 RT "Phylogeny of the Altingiaceae based on cpDNA matK, PY-IGS and nrDNA
 RT ITS sequences.";
 RL Plant Syst. Evol. 230:13-24(2001).
 DR EMBL; AF377996; AAM45514.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
| |::|: |
Db 6 PEPEVKILV 14

RESULT 28

Q8MC23

ID Q8MC23 PRELIMINARY; PRT; 16 AA.
AC Q8MC23;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Sonneratia alba.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Sonneratia.
OX NCBI_TaxID=122812;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S482;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences."
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035741; AAL14163.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
| |::|: |
Db 6 PEPEVKILV 14

RESULT 29

Q8MC41

ID Q8MC41 PRELIMINARY; PRT; 16 AA.
AC Q8MC41;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Nesaea luederitzi.

OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Nesaea.
 OX NCBI_TaxID=162020;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N213;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035732; AAL14145.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

 Query Match 26.8%; Score 22; DB 8; Length 16;
 Best Local Similarity 44.4%; Pred. No. 7.2e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

 Qy 3 PFPKLVKEV 11
 | |::|: |
 Db 6 PEPEVKILV 14

RESULT 30

Q8MC15

ID Q8MC15 PRELIMINARY; PRT; 16 AA.
 AC Q8MC15;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PsAA (Fragment).
 GN PSAA.
 OS Fuchsia hybrid cultivar.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Onagraceae; Fuchsia.
 OX NCBI_TaxID=133545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F016;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035746; AAL14173.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
| |::|: |
Db 6 PEPEVKILV 14

RESULT 31

Q8MC43

ID Q8MC43 PRELIMINARY; PRT; 16 AA.
AC Q8MC43;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Sonneratia caseolaris.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Sonneratia.
OX NCBI_TaxID=122814;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S435;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035731; AAL14143.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
| |::|: |
Db 6 PEPEVKILV 14

RESULT 32

Q8MC47

ID Q8MC47 PRELIMINARY; PRT; 16 AA.
AC Q8MC47;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Peplis portula.

OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Peplis.
 OX NCBI_TaxID=162016;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P220;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035726; AAL14133.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
 Best Local Similarity 44.4%; Pred. No. 7.2e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
 | |::|: |
 Db 6 PEPEVKILV 14

RESULT 33

Q8MC37

ID Q8MC37 PRELIMINARY; PRT; 16 AA.
 AC Q8MC37;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PsaA (Fragment).
 GN PSAA.
 OS Lawsonia inermis.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Lawsonia.
 OX NCBI_TaxID=141191;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L494;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035734; AAL14149.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
| |::|: |
Db 6 PEPEVKILV 14

RESULT 34

Q8MC29

ID Q8MC29 PRELIMINARY; PRT; 16 AA.
AC Q8MC29;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Duabanga grandiflora.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Lythraceae; Duabanga.
OX NCBI_TaxID=122808;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D441;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035738; AAL14157.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
Best Local Similarity 44.4%; Pred. No. 7.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
| |::|: |
Db 6 PEPEVKILV 14

RESULT 35

Q8MC31

ID Q8MC31 PRELIMINARY; PRT; 16 AA.
AC Q8MC31;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Lagerstroemia speciosa.

OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Lagerstroemia.
 OX NCBI_TaxID=122810;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L477;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035737; AAL14155.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
 Best Local Similarity 44.4%; Pred. No. 7.2e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
 | |::|: |
 Db 6 PEPEVKILV 14

RESULT 36

Q8MES8

ID Q8MES8 PRELIMINARY; PRT; 16 AA.
 AC Q8MES8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PSI P700 apoprotein A1 (Fragment).
 GN PSAA.
 OS Daphniphyllum calycinum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Saxifragales; Daphniphyllaceae; Daphniphyllum.
 OX NCBI_TaxID=182071;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;
 RT "Phylogeny of the Altingiaceae based on cpDNA matK, PY-IGS and nrDNA
 RT ITS sequences.";
 RL Plant Syst. Evol. 230:13-24(2001).
 DR EMBL; AF377997; AAM45516.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
 Best Local Similarity 44.4%; Pred. No. 7.2e+03;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
 | |::|: |
 Db 6 PEPEVKILV 14

RESULT 37

Q8MC35

ID Q8MC35 PRELIMINARY; PRT; 16 AA.
 AC Q8MC35;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PsaA (Fragment).
 GN PSAA.
 OS Heimia myrtifolia.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Lythraceae; Heimia.
 OX NCBI_TaxID=135798;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H491;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035735; AAL14151.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 16;
 Best Local Similarity 44.4%; Pred. No. 7.2e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11
 | |::|: |
 Db 6 PEPEVKILV 14

RESULT 38

Q94F61

ID Q94F61 PRELIMINARY; PRT; 16 AA.
 AC Q94F61;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Prolamin-box binding factor (Fragment).
 GN PBF.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Cheyenne;
 RA Chen Z., Fleming J., Zhi Y., Yi M.;
 RT "Sequence of the prolamin-box binding factor (PBF) promoter sequence
 RT from wheat."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF385139; AAK64285.1; -.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1770 MW; B406423B4FFEF76B CRC64;

Query Match 26.8%; Score 22; DB 10; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EVFP 13
 ||||
 Db 3 EVFP 6

RESULT 39

Q9XQN9

ID Q9XQN9 PRELIMINARY; PRT; 17 AA.
 AC Q9XQN9;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Photosystem I P700 chlorophyll (Fragment).
 GN PSAA.
 OS Sinapis alba (White mustard) (Brassica hirta).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Sinapis.
 OX NCBI_TaxID=3728;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cotyledon;
 RX MEDLINE=20136375; PubMed=10672444;
 RA Summer H., Pfannschmidt T., Link G.;
 RT "Transcripts and sequence elements suggest differential promoter usage
 RT within the ycf3-psaAB gene cluster on mustard (Sinapis alba L.)
 RT chloroplast DNA."
 RL Curr. Genet. 37:45-52(2000).
 DR EMBL; AJ242660; CAB45538.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 2008 MW; 99517FE691B89355 CRC64;

Query Match 26.8%; Score 22; DB 8; Length 17;
 Best Local Similarity 44.4%; Pred. No. 7.7e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PFPKLVKEV 11

Db | |::|: |
6 PEPEVKILV 14

RESULT 40

Q8X4A4

ID Q8X4A4 PRELIMINARY; PRT; 17 AA.
AC Q8X4A4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein z4331.
GN Z4331.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamosis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
DR EMBL; AE005528; AAG58115.1; -.
DR PIR; G85956; G85956.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 17 AA; 1823 MW; 5A1C41BC7EF69D69 CRC64;

Query Match 26.8%; Score 22; DB 16; Length 17;
Best Local Similarity 80.0%; Pred. No. 7.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 VFPPF 15
| | | |
Db 4 VSPFP 8

RESULT 41

Q9R8R9

ID Q9R8R9 PRELIMINARY; PRT; 13 AA.
AC Q9R8R9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE C5a peptidase (Fragment).
GN SCPA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=AP1;
 RX MEDLINE=98298075; PubMed=9632622;
 RA Berge A., Rasmussen M., Bjorck L.;
 RT "Identification of an insertion sequence located in a region encoding
 RT virulence factors of Streptococcus pyogenes.";
 RL Infect. Immun. 66:3449-3453(1998).
 DR EMBL; AF064540; AAC38768.1; -.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1603 MW; 5EDADCDA6CEE6723 CRC64;

Query Match 25.6%; Score 21; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 8.7e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKL 7
 || ||
 Db 8 PFDKL 12

RESULT 42

P78359

ID P78359 PRELIMINARY; PRT; 14 AA.
 AC P78359;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NF-kappa-B transcription factor p65 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Umbilical vein;
 RA Remacle J.E., Brys R., Pype S., Nelles L., Huylebroeck D.;
 RT "5' cDNA sequence RelA isolated from Human umbilical vein endothelial
 RT cells.";
 RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U88316; AAB48487.1; -.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

Query Match 25.6%; Score 21; DB 4; Length 14;
 Best Local Similarity 62.5%; Pred. No. 9.4e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Qy 10 EVFP--FP 15
 |:|| ||
 Db 3 ELFPLIFP 10

RESULT 43

Q9HCX8

ID Q9HCX8 PRELIMINARY; PRT; 15 AA.
 AC Q9HCX8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE cAMP-specific phosphodiesterase 4D.
 GN PDE4DN1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20374482; PubMed=10913353;
 RA Miro X., Casacuberta J.M., Gutierrez-Lopez M.D., Landazuri M.O.,
 RA Puigdomenech P.;
 RT "Phosphodiesterases 4D and 7A splice variants in the response of HUVEC
 RT cells to TNF-alpha1.";
 RL Biochem. Biophys. Res. Commun. 274:415-421(2000).
 DR EMBL; AJ250852; CAC03756.1; -.
 DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; NAS.
 DR GO; GO:0009187; P:cyclic nucleotide metabolism; ISS.
 SQ SEQUENCE 15 AA; 1972 MW; 36C1CF0521236FEE CRC64;

Query Match 25.6%; Score 21; DB 4; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1e+04;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LKVEVFPPF 14
 : | |||
 Db 2 MHVNNFPPF 9

RESULT 44

Q44610

ID Q44610 PRELIMINARY; PRT; 16 AA.
 AC Q44610;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Shikimate dehydrogenase (Fragment).
 GN AROE.
 OS Buchnera aphidicola.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95212914; PubMed=7535281;
 RA Rouhbakhsh D., Baumann P.;
 RT "Characterization of a putative 23S-5S rRNA operon of Buchnera
 RT aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding
 RT gene.";
 RL Gene 155:107-112(1995).
 DR EMBL; U10499; AAA79128.1; -.
 DR PIR; I40065; I40065.
 FT NON_TER 1 1
 SQ SEQUENCE 16 AA; 1891 MW; 72A8175598D30DF1 CRC64;

Query Match 25.6%; Score 21; DB 2; Length 16;

Best Local Similarity 60.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPKLK 8
|||::
Db 9 FPKIE 13

RESULT 45

Q9UD41

ID Q9UD41 PRELIMINARY; PRT; 16 AA.
AC Q9UD41;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Beta-isoform thyroid hormone receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95105146; PubMed=7528740;
RA Flynn T.R., Hollenberg A.N., Cohen O., Menke J.B., Usala S.J.,
RA Tollin S., Hegarty M.K., Wondisford F.E.;
RT "A novel C-terminal domain in the thyroid hormone receptor selectively
mediates thyroid hormone inhibition."
RL J. Biol. Chem. 269:32713-32716(1994).
SQ SEQUENCE 16 AA; 1920 MW; 79A831A4F3C8E22F CRC64;

Query Match 25.6%; Score 21; DB 4; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FPKLKVEV 11
:|||::|
Db 2 WPKLLMKV 9

RESULT 46

Q9UC23

ID Q9UC23 PRELIMINARY; PRT; 17 AA.
AC Q9UC23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 25 kDa NKEF-B homolog/thiol-dependent antioxidant protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=96125327; PubMed=8554614;
RA Cha M.K., Kim I.H.;
RT "Thioredoxin-linked peroxidase from human red blood cell: evidence for
the existence of thioredoxin and thioredoxin reductase in human red

RT blood cell.";
RL Biochem. Biophys. Res. Commun. 217:900-907(1995).
SQ SEQUENCE 17 AA; 1657 MW; 75A500A3928D895D CRC64;

Query Match 25.6%; Score 21; DB 4; Length 17;
Best Local Similarity 57.1%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPFPKLLK 8
|| | |
Db 3 KPAPDFK 9

RESULT 47

Q9PS07

ID Q9PS07 PRELIMINARY; PRT; 10 AA.
AC Q9PS07;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Angiotensin I, ANG I.
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RX MEDLINE=93307610; PubMed=8319878;
RA Takei Y., Silldorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,
RA Stephens G.A., Sakakibara S.;
RT "New angiotensin I isolated from a reptile, Alligator
RT mississippiensis.";
RL Gen. Comp. Endocrinol. 90:214-219(1993).
SQ SEQUENCE 10 AA; 1216 MW; CEE38DD761F2DB42 CRC64;

Query Match 24.4%; Score 20; DB 13; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 KVEVFPPF 14
:| | |
Db 2 RVYVHPF 8

RESULT 48

Q36668

ID Q36668 PRELIMINARY; PRT; 12 AA.
AC Q36668;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chloroplast subunit of light independent protochlorophyllide reductase
DE (Fragment).
GN CHLB.
OS Pinus sylvestris (Scots pine).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3349;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cotyledon;
 RX MEDLINE=97263785; PubMed=9108142;
 RA Karpinska B., Karpinski S., Hallgren J.E.;
 RT "The chlB gene encoding a subunit of light-independent
 RT protochlorophyllide reductase is edited in chloroplast of conifers."
 RL Curr. Genet. 31:343-347(1997).
 DR EMBL; X98683; CAA67240.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1445 MW; 0AB0FC0CC2276724 CRC64;

Query Match 24.4%; Score 20; DB 8; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LKPFKPKLK 8
 || || :
 Db 3 LKNLPKAR 10

RESULT 49

Q37791

ID Q37791 PRELIMINARY; PRT; 12 AA.
 AC Q37791;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Chloroplast subunit of light independent protochlorophyllide reductase
 DE (Fragment).
 GN CHLB.
 OS Larix eurolepis.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Larix.
 OX NCBI_TaxID=49226;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cotyledon;
 RA Karpinska B., Karpinski S., Hilgren J.E.;
 RL Curr. Genet. 0:0-0(0).
 DR EMBL; X98686; CAA67244.1; -.
 DR EMBL; X98681; CAA67239.1; -.
 DR EMBL; X98679; CAA67237.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1445 MW; 0AB0FC0CC2276724 CRC64;

Query Match 24.4%; Score 20; DB 8; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LKPFPKLK 8
|| || :
Db 3 LKNLPKAR 10

RESULT 50

Q52636

ID Q52636 PRELIMINARY; PRT; 14 AA.
AC Q52636;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE TraL protein (Fragment).
GN TRAL.
OS Escherichia coli.
OG Plasmid R124.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86059219; PubMed=2999074;
RA Frost L.S., Finlay B.B., Opgenorth A., Paranchych W., Lee J.S.;
RT "Characterization and sequence analysis of pilin from F-like
RT plasmids."
RL J. Bacteriol. 164:1238-1247(1985).
DR EMBL; K03092; AAA92759.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1713 MW; 5CCA91188EB30E23 CRC64;

Query Match 24.4%; Score 20; DB 2; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.4e+04;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 KLKVEVFP 13
||| ||
Db 7 KLKKYRFP 14

Search completed: July 4, 2004, 04:45:41
Job time : 27.5224 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:26 ; Search time 5.14925 Seconds
 (without alignments)
 151.683 Million cell updates/sec

Title: US-09-641-802-8
 Perfect score: 82
 Sequence: 1 LKPFPKLKVEVFPEP 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 952

Minimum DB seq length: 7
 Maximum DB seq length: 18

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	23	28.0	16	1	FOR2_MYRGU	P81437 myrmecia gu
2	21	25.6	11	1	BPPB_AGKHA	P01021 agkistrodon
3	21	25.6	13	1	PEDI_HYDAT	P80578 hydra atten
4	21	25.6	17	1	GPX4_PINPS	P81087 pinus pinas
5	20	24.4	10	1	ANG1_BOTJA	Q10581 bothrops ja
6	20	24.4	10	1	ANGT_BOVIN	P01017 bos taurus
7	20	24.4	10	1	ANGT_CHICK	P01018 gallus gall
8	20	24.4	11	1	ANGT_CRIGE	P09037 crinia geor
9	20	24.4	13	1	NP5_LYMST	P80182 lymnaea sta
10	20	24.4	15	1	LPF_ECOLI	P03057 escherichia
11	19	23.2	8	1	ANG2_BOTJA	Q10582 bothrops ja
12	19	23.2	10	1	PVK_LOCMI	P83382 locusta mig
13	19	23.2	11	1	CSI5_BACSU	P81095 bacillus su
14	19	23.2	12	1	UH03_RAT	P56572 rattus norv
15	19	23.2	13	1	NP4_LYMST	P80181 lymnaea sta
16	19	23.2	14	1	ANGT_HORSE	P01016 equus cabal
17	19	23.2	15	1	MK2A_PALPR	P80409 palomena pr

18	19	23.2	16	1	FOR1_MYRGU	P81438	myrmecia gu
19	19	23.2	16	1	MK2B_PALPR	P80410	palomena pr
20	19	23.2	16	1	MK3_PALPR	P80411	palomena pr
21	19	23.2	17	1	APID_BOMPA	P81464	bombus pasc
22	18	22.0	13	1	IDHP_RAT	P56574	rattus norv
23	18	22.0	15	1	RBS_PHYPA	P80657	physcomitre
24	18	22.0	16	1	LEC_DELRE	P83511	delonix reg
25	18	22.0	17	1	TL09_SPIOL	P82671	spinacia ol
26	18	22.0	18	1	UC21_MAIZE	P80627	zea mays (m
27	17.5	21.3	8	1	PPK3_PERAM	P82618	periplaneta
28	17.5	21.3	15	1	UC25_MAIZE	P80631	zea mays (m
29	17	20.7	8	1	RS7_MYCIT	P33564	mycobacteri
30	17	20.7	10	1	BPP_VIPAS	P31351	vipera aspi
31	17	20.7	10	1	PNEU_HUMAN	P22103	homo sapien
32	17	20.7	10	1	PNEU_RAT	P21996	rattus norv
33	17	20.7	10	1	SLAP_BACTG	P49325	bacillus th
34	17	20.7	11	1	TKNA_GADMO	P28498	gadus morhu
35	17	20.7	11	1	TKNA_RANCA	P22688	rana catesb
36	17	20.7	11	1	TKNA_RANRI	P29207	rana ridibu
37	17	20.7	11	1	TKND_RANCA	P22691	rana catesb
38	17	20.7	13	1	MP1_MICOC	P81532	microplitis
39	17	20.7	13	1	NP2_LYMST	P80179	lymnaea sta
40	17	20.7	13	1	YPE2_LACLC	P42021	lactococcus
41	17	20.7	14	1	IF2G_RAT	P81795	rattus norv
42	17	20.7	14	1	UC34_MAIZE	P80640	zea mays (m
43	17	20.7	15	1	GTS_ASADI	P83246	asaphis dic
44	17	20.7	15	1	UC17_MAIZE	P80623	zea mays (m
45	17	20.7	15	1	UC29_MAIZE	P80635	zea mays (m
46	17	20.7	17	1	H2B3 ICTPU	P81904	ictalurus p
47	16.5	20.1	9	1	LMT3_LOCFI	P41489	locusta mig
48	16.5	20.1	15	1	UBL1_MONDO	P50103	monodelphis
49	16.5	20.1	16	1	LPK1_LOCFI	P20404	locusta mig
50	16	19.5	10	1	BPP2_BOTIN	P30422	bothrops in
51	16	19.5	11	1	BRK_MEGFL	P12797	megascolia
52	16	19.5	11	1	OAIIF_SARBU	P83518	sarcophaga
53	16	19.5	11	1	Q2OA_COMTE	P80464	comamonas t
54	16	19.5	11	1	TIN1_HOPTI	P82651	hoplobatrach
55	16	19.5	11	1	TKNA_ONCFI	P28499	oncorhynchus
56	16	19.5	11	1	TKNA_SCYCA	P41333	scyliorhinu
57	16	19.5	12	1	XYLA_STRVN	P14405	streptomyces
58	16	19.5	13	1	BPP1_BOTJA	P01020	bothrops ja
59	16	19.5	13	1	BRK_PARID	P42717	parapolybia
60	16	19.5	13	1	FIBB_RABIT	P14478	oryctolagus
61	16	19.5	13	1	NP1_LYMST	P80178	lymnaea sta
62	16	19.5	13	1	NP3_LYMST	P80180	lymnaea sta
63	16	19.5	14	1	LPER_BACLI	Q04303	bacillus li
64	16	19.5	14	1	MARI_ALTSP	P29399	alteromonas
65	16	19.5	15	1	AF1L_MALPA	P83141	malva parvi
66	16	19.5	15	1	FGF1_CANFA	P18651	canis famill
67	16	19.5	15	1	MCRA_METTE	P22948	methanosarc
68	16	19.5	15	1	VORA_METTM	P80907	methanobact
69	16	19.5	16	1	H5_COTJA	P18638	coturnix co
70	16	19.5	16	1	MMPX_SOLTU	P80501	solanum tub
71	15.5	18.9	8	1	PPK2_PERAM	P82692	periplaneta
72	15.5	18.9	13	1	LMT4_LOCFI	P41490	locusta mig
73	15.5	18.9	16	1	AF1S_MALPA	P83140	malva parvi
74	15.5	18.9	16	1	ODO2_BOVIN	P11179	bos taurus

75	15	18.3	8	1	B44K_PORGI	P81886	porphyromon
76	15	18.3	9	1	MGMT_BOVIN	P29177	bos taurus
77	15	18.3	10	1	UPA5_HUMAN	P30091	homo sapien
78	15	18.3	13	1	CRBL_ICASP	P17237	icaria sp.
79	15	18.3	13	1	TY13_PHYRO	P04096	phyllomedus
80	15	18.3	15	1	CBPB_PROAT	P19628	protopterus
81	15	18.3	15	1	MK1_PALPR	P80408	palomena pr
82	15	18.3	15	1	UP02_METAN	P83439	metarhizium
83	15	18.3	16	1	DHE2_THUTH	P20016	thunnus thy
84	15	18.3	17	1	SRY_URSAR	P36396	ursus arcto
85	15	18.3	17	1	UP33_UPEIN	P82034	uperoleia i
86	15	18.3	17	1	YALA_TRYBB	P17961	trypanosoma
87	15	18.3	18	1	PDHC_ORCLI	P83587	orconectes
88	14.5	17.7	15	1	HS11_PINPS	P81083	pinus pinas
89	14	17.1	9	1	COXE_THUOB	P80975	thunnus obe
90	14	17.1	9	1	FAR5_PENMO	P83320	penaeus mon
91	14	17.1	9	1	FLA2_TREHY	P80159	treponema h
92	14	17.1	9	1	UPA3_HUMAN	P30089	homo sapien
93	14	17.1	10	1	BPP2_BOTJA	P01022	bothrops ja
94	14	17.1	10	1	COXA_ONCMY	P80328	oncorhynchu
95	14	17.1	10	1	FAR6_PANRE	P82660	panagrellus
96	14	17.1	10	1	GAJU_HUMAN	P01358	homo sapien
97	14	17.1	11	1	BPP3_BOTIN	P30423	bothrops in
98	14	17.1	11	1	BPP4_BOTIN	P30424	bothrops in
99	14	17.1	11	1	BPP_AGKHP	P04562	agkistrodon
100	14	17.1	11	1	TIN4_HOPTI	P82654	hoplobatrach

ALIGNMENTS

RESULT 1

FOR2_MYRGU

ID FOR2_MYRGU STANDARD; PRT; 16 AA.
AC P81437;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Formaecin 2.
OS Myrmecia gulosa (Red bulldog ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Formicidae; Myrmeciinae; Myrmecini; Myrmecia.
OX NCBI_TaxID=36170;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RC TISSUE=Hemolymph;
RX MEDLINE=98165787; PubMed=9497332;
RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
RT "Isolation from an ant Myrmecia gulosa of two inducible
RT O-glycosylated proline-rich antibacterial peptides.";
RL J. Biol. Chem. 273:6139-6143(1998).
CC -!- FUNCTION: Antibacterial peptide. Has activity against E.coli but
CC none against other Gram-negative bacteria and Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By bacterial infection.

CC -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-
 CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
 CC -!- SIMILARITY: TO DROSOPHILA DROSOCIN.
 KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
 FT CARBOHYD 11 11 O-LINKED (GALNAC. . .).
 SQ SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BC2E0AE CRC64;

Query Match 28.0%; Score 23; DB 1; Length 16;
 Best Local Similarity 60.0%; Pred. No. 8.4e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFPKL 7
 | : | : |
 Db 12 PYPRL 16

RESULT 2

BPPB_AGKHA

ID BPPB_AGKHA STANDARD; PRT; 11 AA.
 AC P01021;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide B (Angiotensin-converting
 DE enzyme inhibitor).
 OS Agkistrodon halys blomhoffii (Mamushi) (Gloydius blomhoffii).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 OX NCBI_TaxID=242054;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Kato H., Suzuki T.;
 RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
 RT the venom of Agkistrodon halys blomhoffii.";
 RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A01254; XASNBA.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 25.6%; Score 21; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 1.2e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKPFPKL 7
 | | | : |
 Db 3 LPPRPKI 9

RESULT 3

PEDI_HYDAT

ID PEDI_HYDAT STANDARD; PRT; 13 AA.
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pedin.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE.
RX MEDLINE=96232307; PubMed=8674432;
RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
RT peptides from Hydra vulgaris.";
RL Development 122:1941-1948(1996).
CC -!- FUNCTION: Morphogenetically active peptide. Active in foot
CC development.
KW Morphogen.
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 25.6%; Score 21; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 KLKVEVFP 13
:|: || |
Db 2 ELRPEVLP 9

RESULT 4

GPX4_PINPS

ID GPX4_PINPS STANDARD; PRT; 17 AA.
AC P81087;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Glutathione peroxidase homolog (EC 1.11.1.9) (Water stress responsive
DE proteins 8 and 9) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;

RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
 CC glutathione + 2 H(2)O.
 CC -!- INDUCTION: By water stress.
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein is:
 CC 5.6 to 6.7, its MW is: 20 to 23 kDa.
 CC -!- SIMILARITY: Belongs to the glutathione peroxidase family.
 DR InterPro; IPR000889; Glut_peroxidase.
 DR Pfam; PF00255; GSHPx; 1.
 DR PROSITE; PS00460; GLUTATHIONE_PEROXID_1; PARTIAL.
 DR PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Peroxidase; Oxidoreductase.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1943 MW; 4D245E9B657868C1 CRC64;

Query Match 25.6%; Score 21; DB 1; Length 17;
 Best Local Similarity 42.9%; Pred. No. 1.9e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 9 VEVFPFP 15
 :|: ||
 Db 6 LEILAFP 12

RESULT 5

ANG1_BOTJA

ID ANG1_BOTJA STANDARD; PRT; 10 AA.
 AC Q10581;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide I (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake Bothrops jararaca."
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -!- SIMILARITY: Belongs to the serpin family.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 24.4%; Score 20; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 1.6e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KVEVFPF 14
:| | |
Db 2 RVYVHPF 8

RESULT 6

ANGT_BOVIN

ID ANGT_BOVIN STANDARD; PRT; 10 AA.
AC P01017;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
DE (Fragment).
GN AGT OR SERPINA8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Elliott D.F., Peart W.S.;
RT "The amino acid sequence in a hypertensin.";
RL Biochem. J. 65:246-254(1957).
CC -!- FUNCTION: In response to lowered blood pressure, the enzyme renin
CC cleaves angiotensin I, from angiotensinogen. ACE (angiotensin
CC converting enzyme) then removes a dipeptide to yield the
CC physiologically active peptide angiotensin II, the most potent
CC pressor substance known, which helps regulate volume and mineral
CC balance of body fluids.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -!- SIMILARITY: Belongs to the serpin family.
DR PIR; A90345; A90345.
DR PDB; 3ER5; 15-JUL-92.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1282 MW; CEEFBDD761F2DB42 CRC64;

Query Match 24.4%; Score 20; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KVEVFPF 14
:| | |
Db 2 RVYVHPF 8

RESULT 7

ANGT_CHICK

ID ANGT_CHICK STANDARD; PRT; 10 AA.
AC P01018;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
DE (Fragment).
GN AGT OR SERPINA8.
OS Gallus gallus (Chicken), and
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031, 93934;
RN [1]
RP SEQUENCE.
RC SPECIES=Chicken;
RX MEDLINE=74127845; PubMed=4361802;
RA Nakayama T., Nakajima T., Sokabe H.;
RT "Comparative studies on angiotensins. 3. Structure of fowl
RT angiotensin and its identification by DNS-method.";
RL Chem. Pharm. Bull. 21:2085-2087(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C.c.japonica;
RX MEDLINE=90284684; PubMed=2191893;
RA Takei Y., Hasegawa Y.;
RT "Vasopressor and depressor effects of native angiotensins and
RT inhibition of these effects in the Japanese quail.";
RL Gen. Comp. Endocrinol. 79:12-22(1990).
CC -!- FUNCTION: In response to lowered blood pressure, the enzyme renin
CC cleaves angiotensin I, from angiotensinogen. ACE (angiotensin
CC converting enzyme) then removes a dipeptide to yield the
CC physiologically active peptide angiotensin II, the most potent
CC pressor substance known, which helps regulate volume and mineral
CC balance of body fluids.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -!- SIMILARITY: Belongs to the serpin family.
DR PIR; A60624; A60624.
DR PIR; A90917; A90917.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1232 MW; CEFBEDD761F2DB42 CRC64;

Query Match 24.4%; Score 20; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KVEVFPF 14
:| | |
Db 2 RVYVHPF 8

RESULT 8

ANGT_CRIGE

ID ANGT_CRIGE STANDARD; PRT; 11 AA.
AC P09037;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Crinia-angiotensin II.
OS Crinia georgiana (Quacking frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Crinia.
OX NCBI_TaxID=8374;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=80024575; PubMed=488254;
RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
RT "Amino acid composition and sequence of crinia-angiotensin, an
RT angiotensin II-like endecapeptide from the skin of the Australian
RT frog Crinia georgiana.";
RL Experientia 35:1132-1133(1979).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; S07207; S07207.
KW Vasoconstrictor.
SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 24.4%; Score 20; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PKLKVEVFPF 14
| :: | |
Db 2 PGDRIYVHPF 11

RESULT 9

NP5_LYMST

ID NP5_LYMST STANDARD; PRT; 13 AA.
AC P80182;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymna-DF-amide 5.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;

RX MEDLINE=93238777; PubMed=8477756;
 RA Johnsen A.H., Rehfeld J.F.;
 RT "LymnaeDFamides, a new family of neuropeptides from the pond snail,
 RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
 RT invertebrates?";
 RL Eur. J. Biochem. 213:875-879(1993).
 CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
 DR PIR; S32475; S32475.
 KW Neuropeptide; Amidation.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1476 MW; 9CA07BBB56D5A5A5 CRC64;

Query Match 24.4%; Score 20; DB 1; Length 13;
 Best Local Similarity 30.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PFPKLVKVEVF 12
 || :: |
 Db 1 PFDRISSSAF 10

RESULT 10
 LPF_ECOLI
 ID LPF_ECOLI STANDARD; PRT; 15 AA.
 AC P03057;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Phe leader peptide (Attenuator peptide).
 GN PHEL OR PHEAE OR B2598 OR SF2658 OR S4807.
 OS Escherichia coli, and
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562, 623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli;
 RX MEDLINE=79033820; PubMed=360214;
 RA Zurawski G., Brown K., Killingly D., Yanofsky C.;
 RT "Nucleotide sequence of the leader region of the phenylalanine operon
 RT of Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:4271-4275(1978).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli;
 RX MEDLINE=91072346; PubMed=2254312;
 RA Gavini N., Davidson B.E.;
 RT "pheAo mutants of Escherichia coli have a defective pheA attenuator.";
 RL J. Biol. Chem. 265:21532-21535(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; PubMed=12384590;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RT through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
 RX MEDLINE=22590274; PubMed=12704152;
 RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
 RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
 RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
 RA Schwartz D.C., Blattner F.R.;
 RT "Complete genome sequence and comparative genomics of Shigella
 RT flexneri serotype 2a strain 2457T.";
 RL Infect. Immun. 71:2775-2786(2003).
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 CC OF PHENYLALANINE.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; V00314; CAA23600.1; -.
 DR EMBL; M10431; AAA24329.1; -.
 DR EMBL; M58024; AAA62783.1; -.
 DR EMBL; AE000346; AAC75647.1; -.
 DR EMBL; AE015281; AAN44154.1; -.
 DR EMBL; AE016987; AAP17979.1; -.
 DR PIR; A03593; LFECF.
 DR EcoGene; EG11271; pheL.
 KW Leader peptide; Complete proteome.
 SQ SEQUENCE 15 AA; 1924 MW; CFE14AE3BFF935E0 CRC64;

Query Match 24.4%; Score 20; DB 1; Length 15;
 Best Local Similarity 33.3%; Pred. No. 2.4e+03;
 Matches 5; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 LKPFPKLKVEVFPPF 15
 :| | | ||
 Db 1 MKHIPFFFAFFFTFP 15

RESULT 11

ANG2_BOTJA

ID ANG2_BOTJA STANDARD; PRT; 8 AA.
 AC Q10582;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide II (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake Bothrops jararaca."
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -!- SIMILARITY: Belongs to the serpin family.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 23.2%; Score 19; DB 1; Length 8;
 Best Local Similarity 42.9%; Pred. No. 1.4e+05;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KVEVFPPF 14
 :| : ||
 Db 2 RVYIHPF 8

RESULT 12

PVK_LOCFI

ID PVK_LOCFI STANDARD; PRT; 10 AA.
 AC P83382;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Periviscerokinin (Lom-PVK-1).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Abdominal perisymphathetic organs;
 RX MEDLINE=21896327; PubMed=11897380;
 RA Predel R., Gaede G.;
 RT "Identification of the abundant neuropeptide from abdominal
 RT perisymphathetic organs of locusts.";

RL Peptides 23:621-627(2002).
 CC -!- FUNCTION: Myotropic peptide; increases the frequency of
 CC contraction of the heart and stimulates amplitude and tonus of the
 CC foregut.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.
 DR GO; GO:0005576; C:extracellular; IDA.
 DR GO; GO:0005184; F:neuropeptide hormone activity; IDA.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
 KW Neuropeptide; Amidation.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;

Query Match 23.2%; Score 19; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 VFPPF 15
 :| ||
 Db 4 LFQFP 8

RESULT 13
 CSI5_BACSU
 ID CSI5_BACSU STANDARD; PRT; 11 AA.
 AC P81095;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=168 / JH642;
 RA Graumann P.L., Schmid R., Marahiel M.A.;
 RL Submitted (OCT-1997) to Swiss-Prot.
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=168 / JH642;
 RX MEDLINE=96345629; PubMed=8755892;
 RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
 RT "Cold shock stress-induced proteins in Bacillus subtilis."
 RL J. Bacteriol. 178:4611-4619(1996).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- INDUCTION: In response to low temperature.
 CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 23.2%; Score 19; DB 1; Length 11;
 Best Local Similarity 75.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPF 4
 :|||

RESULT 14

UH03_RAT

ID UH03_RAT STANDARD; PRT; 12 AA.
AC P56572;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P3) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 8.3, its MW is: 28 kDa.
FT UNSURE 2 2
FT UNSURE 9 9
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1255 MW; 46F58D101DC33053 CRC64;

Query Match 23.2%; Score 19; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KLKVEV 11
|:| |
Db 5 KIKVAV 10

RESULT 15

NP4_LYMST

ID NP4_LYMST STANDARD; PRT; 13 AA.
AC P80181;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymna-DF-amide 4.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeoidea; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RT "LymnaDFamides, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";

RL Eur. J. Biochem. 213:875-879(1993).
 CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
 DR PIR; S32474; S32474.
 KW Neuropeptide; Amidation.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1503 MW; 9CA07BBB56D5B455 CRC64;

Query Match 23.2%; Score 19; DB 1; Length 13;
 Best Local Similarity 30.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PFPKLKVEVF 12
 || :: |
 Db 1 PFDRISNSAF 10

RESULT 16

ANGT_HORSE

ID ANGT_HORSE STANDARD; PRT; 14 AA.
 AC P01016;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
 DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
 DE (Fragment).
 GN AGT OR SERPINA8.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE.
 RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
 RT "The preparation, purification, and amino acid sequence of a
 RT polypeptide renin substrate."
 RL J. Exp. Med. 106:439-453(1957).
 CC -!- FUNCTION: In response to lowered blood pressure, the enzyme renin
 CC cleaves angiotensin I, from angiotensinogen. ACE (angiotensin
 CC converting enzyme) then removes a dipeptide to yield the
 CC physiologically active peptide angiotensin II, the most potent
 CC pressor substance known, which helps regulate volume and mineral
 CC balance of body fluids.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -!- SIMILARITY: Belongs to the serpin family.
 DR PIR; A92775; A01250.
 DR PDB; 1ER8; 15-OCT-91.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1759 MW; 2E9921F8EEEFBDD7 CRC64;

Query Match 23.2%; Score 19; DB 1; Length 14;
Best Local Similarity 42.9%; Pred. No. 3.3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KVEVFPP 14
:| : ||
Db 2 RVYIHPF 8

RESULT 17

MK2A_PALPR

ID MK2A_PALPR STANDARD; PRT; 15 AA.
AC P80409;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metalnikowin IIA.
OS Palomena prasina (Green shield bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
OC Palomena.
OX NCBI_TaxID=55431;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect
RT Palomena prasina: identification of a unique family of proline-rich
RT peptides and of a novel insect defensin.";
RL J. Insect Physiol. 42:81-89(1996).
CC -!- FUNCTION: Antibacterial peptide active against Gram-negative
CC bacteria.
CC -!- INDUCTION: By bacterial infection.
KW Antibiotic; Insect immunity.
SQ SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;

Query Match 23.2%; Score 19; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KPFPK 6
:|:|:
Db 9 RPWPR 13

RESULT 18

FOR1_MYRGU

ID FOR1_MYRGU STANDARD; PRT; 16 AA.
AC P81438;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Formaecin 1.
OS Myrmecia gulosa (Red bulldog ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;

OC Formicidae; Myrmeciinae; Myrmeciini; Myrmecia.
 OX NCBI_TaxID=36170;
 RN [1]
 RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
 RC TISSUE=Hemolymph;
 RX MEDLINE=98165787; PubMed=9497332;
 RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
 RT "Isolation from an ant *Myrmecia gulosa* of two inducible
 RT O-glycosylated proline-rich antibacterial peptides.";
 RL J. Biol. Chem. 273:6139-6143(1998).
 CC -!- FUNCTION: Antibacterial peptide. Has activity against *E.coli*
 CC but none against other Gram-negative bacteria and Gram-positive
 CC bacteria.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- INDUCTION: By bacterial infection.
 CC -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-
 CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
 CC -!- SIMILARITY: TO DROSOPHILA DROSOCIN.
 KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
 FT CARBOHYD 11 11 O-LINKED (GALNAC. . .).
 SQ SEQUENCE 16 AA; 1794 MW; 80CEA3AABBC2E0AE CRC64;

Query Match 23.2%; Score 19; DB 1; Length 16;
 Best Local Similarity 60.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKL 7
 | | : |
 Db 12 PHPRL 16

RESULT 19

MK2B_PALPR

ID MK2B_PALPR STANDARD; PRT; 16 AA.
 AC P80410;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Metalnikowin IIB.
 OS *Palomena prasina* (Green shield bug).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
 OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
 OC *Palomena*.
 OX NCBI_TaxID=55431;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 RT *Palomena prasina*: identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin.";
 RL J. Insect Physiol. 42:81-89(1996).
 CC -!- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -!- INDUCTION: By bacterial infection.
 KW Antibiotic; Insect immunity.

SQ SEQUENCE 16 AA; 2040 MW; AF21407D063B9462 CRC64;

Query Match 23.2%; Score 19; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KPFPK 6
:|:|:
Db 9 RPWPR 13

RESULT 20

MK3_PALPR

ID MK3_PALPR STANDARD; PRT; 16 AA.

AC P80411;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Metalnikowin III.

OS Palomena prasina (Green shield bug).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;

OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;

OC Palomena.

OX NCBI_TaxID=55431;

RN [1]

RP SEQUENCE.

RC TISSUE=Hemolymph;

RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;

RT "The inducible antibacterial peptides of the hemipteran insect

RT Palomena prasina: identification of a unique family of proline-rich
peptides and of a novel insect defensin.";

RL J. Insect Physiol. 42:81-89(1996).

CC -!- FUNCTION: Antibacterial peptide active against Gram-negative
bacteria.

CC -!- INDUCTION: By bacterial infection.

KW Antibiotic; Insect immunity.

SQ SEQUENCE 16 AA; 2024 MW; A9E3835D063B9462 CRC64;

Query Match 23.2%; Score 19; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KPFPK 6
:|:|:
Db 9 RPWPR 13

RESULT 21

APID_BOMPA

ID APID_BOMPA STANDARD; PRT; 17 AA.

AC P81464;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Apidaecin.

OS Bombus pascuorum (Brown bumble bee).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 OC Apidae; Bombus.
 OX NCBI_TaxID=65598;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RX MEDLINE=97362903; PubMed=9219367;
 RA Rees J.A., Moniatte M., Bulet P.;
 RT "Novel antibacterial peptides isolated from a European bumblebee,
 RT Bombus pascuorum (Hymenoptera, Apoidea).";
 RL Insect Biochem. Mol. Biol. 27:413-422(1997).
 CC -!- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -!- INDUCTION: By bacterial infection.
 DR InterPro; IPR004828; Apidaecin.
 DR Pfam; PF00807; Apidaecin; 1.
 KW Insect immunity; Antibiotic; Hemolymph.
 SQ SEQUENCE 17 AA; 1963 MW; CD1D0D02C8BC23D1 CRC64;

Query Match 23.2%; Score 19; DB 1; Length 17;
 Best Local Similarity 60.0%; Pred. No. 4e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PFPKL 7
 | | : |
 Db 13 PHPRL 17

RESULT 22

IDHP_RAT
 ID IDHP_RAT STANDARD; PRT; 13 AA.
 AC P56574;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Isocitrate dehydrogenase [NADP], mitochondrial (EC 1.1.1.42)
 DE (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP) (ICD-
 DE M) (Fragment).
 GN IDH2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Heart;
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
 RA Jungblut P.R.;
 RL Submitted (SEP-1998) to Swiss-Prot.
 CC -!- FUNCTION: PLAYS A ROLE IN INTERMEDIARY METABOLISM AND ENERGY
 CC PRODUCTION. IT MAY TIGHTLY ASSOCIATE OR INTERACT WITH THE PYRUVATE
 CC DEHYDROGENASE COMPLEX (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2)
 CC + NADPH.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
 CC (SPOT P8) IS: 9.0, ITS MW IS: 42 kDa.
 CC -!- SIMILARITY: Belongs to the isocitrate and isopropylmalate
 CC dehydrogenases family.
 DR InterPro; IPR001804; Isodh.
 DR PROSITE; PS00470; IDH_IMDH; PARTIAL.
 KW Oxidoreductase; NADP; Glyoxylate bypass; Tricarboxylic acid cycle;
 KW Mitochondrion.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1526 MW; 5FB81031723E02C3 CRC64;

Query Match 22.0%; Score 18; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKVE 10
 :|||
 Db 4 RIKVE 8

RESULT 23

RBS_PHYPA

ID RBS_PHYPA STANDARD; PRT; 15 AA.
 AC P80657;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ribulose biphosphate carboxylase small chain (EC 4.1.1.39) (RuBisCO
 DE small subunit) (Fragment).
 GN RBCS.
 OS Physcomitrella patens (Moss).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 OX NCBI_TaxID=3218;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Protonema;
 RX MEDLINE=97275459; PubMed=9129336;
 RA Kasten B., Buck F., Nuske J., Reski R.;
 RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
 RT plastid enzymes."
 RL Planta 201:261-272(1997).
 CC -!- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
 CC carbon dioxide fixation, as well as the oxidative fragmentation of
 CC the pentose substrate in the photorespiration process. Both
 CC reactions occur simultaneously and in competition at the same
 CC active site.
 CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O =
 CC 2 3-phospho-D-glycerate.
 CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) =
 CC 3-phospho-D-glycerate + 2-phosphoglycolate.
 CC -!- SUBUNIT: 8 large chains + 8 small chains.
 CC -!- SUBCELLULAR LOCATION: Chloroplast.
 CC -!- SIMILARITY: Belongs to the RuBisCO small chain family.
 KW Photosynthesis; Carbon dioxide fixation; Photorespiration;
 KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast.

FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1801 MW; 28B9E7AC4AED6CE0 CRC64;

Query Match 22.0%; Score 18; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 5.1e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PFPKLKVEVF 12
| : | | |
Db 6 PIGQPKFETF 15

RESULT 24

LEC_DELRE

ID LEC_DELRE STANDARD; PRT; 16 AA.

AC P83511;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Lectin (DRL) (Fragment).

OS Delonix regia (Royal poinciana).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids I; Fabales; Fabaceae; Caesalpinioideae; Caesalpinieae;

OC Delonix.

OX NCBI_TaxID=72433;

RN [1]

RP SEQUENCE, AND CHARACTERIZATION.

RC TISSUE=Seed;

RX MEDLINE=22158378; PubMed=12168698;

RA Pando S.C., Macedo M.L.R., Freire M.G.M., Toyama M.H., Novello J.C.,

RA Marangoni S.;

RT "Biochemical characterization of a lectin from Delonix regia seeds.";

RL J. Protein Chem. 21:279-285(2002).

CC -!- FUNCTION: Glucose-specific lectin.

CC -!- SUBUNIT: Monomer.

CC -!- MISCELLANEOUS: Optimal pH is 8.0-9.0. Active up to 60 degrees

CC Celsius.

CC -!- MISCELLANEOUS: Requires manganese but not calcium ions for cell-
agglutinating activity.

CC -!- SIMILARITY: Belongs to the leguminous lectin family.

DR GO; GO:0005536; F:glucose binding; IDA.

DR GO; GO:0030145; F:manganese ion binding; IDA.

DR GO; GO:0016337; P:cell-cell adhesion; IDA.

DR InterPro; IPR001220; Lectin_legB.

DR PROSITE; PS00307; LECTIN_LEGUME_BETA; PARTIAL.

KW Lectin; Glycoprotein; Manganese.

FT NON_TER 16 16

SQ SEQUENCE 16 AA; 1816 MW; D3DA3A36D1C308BE CRC64;

Query Match 22.0%; Score 18; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 EVFPFP 15
| : | |
Db 1 EITKFP 6

RESULT 25

TL09_SPIOL

ID TL09_SPIOL STANDARD; PRT; 17 AA.
 AC P82671;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thylakoid lumenal 9 kDa protein (P9) (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Amaranthaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RA Kieselbach T., Pettersson U., Bystedt M., Schroeder W.P.;
 RL Submitted (MAY-2000) to Swiss-Prot.
 CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
 KW Chloroplast; Thylakoid.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1683 MW; A8B04C2AEFDBCBC1 CRC64;

Query Match 22.0%; Score 18; DB 1; Length 17;
 Best Local Similarity 42.9%; Pred. No. 5.8e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 VEVFPFP 15
 :| | |
 Db 9 IEXIPGP 15

RESULT 26

UC21_MAIZE

ID UC21_MAIZE STANDARD; PRT; 18 AA.
 AC P80627;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 443)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.9, its MW is: 26.5 kDa.

CC -!- SIMILARITY: TO L-ASCORBATE PEROXIDASES.
 DR Maize-2DPAGE; P80627; COLEOPTILE.
 DR MaizeDB; 123953; -.
 FT NON_TER 1 1
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1938 MW; F32F6FEF038BAB8A CRC64;

Query Match 22.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 33.3%; Pred. No. 6.1e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KPFPKLVKVE 10
 | : | : |
 Db 2 KNYPTVSAE 10

RESULT 27

PPK3_PERAM

ID PPK3_PERAM STANDARD; PRT; 8 AA.
 AC P82618;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 RT abdominal neurohemal organs of the American cockroach."
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach."
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
 CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 21.3%; Score 17.5; DB 1; Length 8;
 Best Local Similarity 62.5%; Pred. No. 1.4e+05;
 Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 LKPF-PKL 7
 | | | : |
 Db 1 LVPFRPRL 8

RESULT 28

UC25_MAIZE

ID UC25_MAIZE STANDARD; PRT; 15 AA.
 AC P80631;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 77)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.9, its MW is: 31.6 kDa.
 DR Maize-2DPAGE; P80631; COLEOPTILE.
 DR MaizeDB; 123957; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1580 MW; 83C54CF0CE1614D0 CRC64;

Query Match 21.3%; Score 17.5; DB 1; Length 15;
 Best Local Similarity 45.5%; Pred. No. 6.2e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 2 KPFPKLKVEVF 12
 : | | | | |
 Db 7 RSFP---VEAF 14

RESULT 29

RS7_MYCIT

ID RS7_MYCIT STANDARD; PRT; 8 AA.
 AC P33564;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S7 (Fragment).
 GN RPSG.
 OS Mycobacterium intracellulare.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1767;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93197130; PubMed=8451173;
 RA Nair J., Rouse D.A., Morris S.L.;
 RT "Nucleotide sequence analysis of the ribosomal S12 gene of
 RT Mycobacterium intracellulare.";
 RL Nucleic Acids Res. 21:1039-1039(1993).
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 CC directly to 16S rRNA where it nucleates assembly of the head
 CC domain of the 30S subunit. Is located at the subunit interface
 CC close to the decoding center, probably blocks exit of the E-site
 CC tRNA (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
 CC and S11 (By similarity).
 CC -!- SIMILARITY: Belongs to the S7P family of ribosomal proteins.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L08171; AAA25376.1; -.
 DR PIR; S35538; S35538.
 DR HAMAP; MF_00480; -; 1.
 DR InterPro; IPR000235; Ribosomal_S7.
 DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
 KW Ribosomal protein; RNA-binding; rRNA-binding; tRNA-binding.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match 20.7%; Score 17; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPK 6
 | ||
 Db 5 PAPP 8

RESULT 30

BPP_VIPAS

ID BPP_VIPAS STANDARD; PRT; 10 AA.
 AC P31351;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting
 DE enzyme inhibitor).
 OS Vipera aspis (Aspic viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Vipera.
 OX NCBI_TaxID=8706;

RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90382616; PubMed=2169439;
 RA Komori Y., Sugihara H.;
 RT "Characterization of a new inhibitor for angiotensin converting
 RT enzyme from the venom of *Vipera aspis aspis*.";
 RL Int. J. Biochem. 22:767-771(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A60377; XASNPC.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 20.7%; Score 17; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKL 7
 | ||:
 Db 4 PGPKV 8

RESULT 31

PNEU_HUMAN

ID PNEU_HUMAN STANDARD; PRT; 10 AA.
 AC P22103;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pneumadin (PNM).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=91110910; PubMed=2274681;
 RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
 RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
 RL Regul. Pept. 30:77-87(1990).
 CC -!- FUNCTION: Antidiuretic peptide that triggers the release of ADH.
 DR PIR; B33143; B33143.
 DR GO; GO:0030103; P:vasopressin secretion; NAS.
 KW Amidation.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match 20.7%; Score 17; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 5e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEV 11

Db ||| |
 4 PKLDAGV 10

RESULT 32

PNEU_RAT

ID PNEU_RAT STANDARD; PRT; 10 AA.
AC P21996;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNM).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis."
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: This antidiuretic peptide triggers the release of ADH.
DR PIR; A33143; A33143.
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

Query Match 20.7%; Score 17; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 5e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PKLKVEV 11
 ||| |
Db 4 PKLDAGV 10

RESULT 33

SLAP_BACTG

ID SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL 4045;
RX MEDLINE=90078111; PubMed=2592346;
RA Luckevich M.D., Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis."
RL J. Bacteriol. 171:6656-6667(1989).
CC -!- FUNCTION: The S-layer is a paracrystalline mono-layered assembly

CC of proteins which coat the surface of bacteria.
 CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
 CC S-LAYER WITH OBLIQUE (P2) SYMMETRY.
 DR PIR; A60476; A60476.
 KW Cell wall; S-layer.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;

Query Match 20.7%; Score 17; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KPFP 5
 | ||
 Db 3 KTFP 6

RESULT 34

TKNA_GADMO
 ID TKNA_GADMO STANDARD; PRT; 11 AA.
 AC P28498;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Gadus morhua (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
 OX NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout.";
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S23306; S23306.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 20.7%; Score 17; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KPFPK 6
|| |:
Db 1 KPRPQ 5

RESULT 35

TKNA_RANCA

ID TKNA_RANCA STANDARD; PRT; 11 AA.
AC P22688;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin A (RTK A).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain, and Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT intestine.";
RL Regul. Pept. 46:81-88(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A61033; A61033.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 20.7%; Score 17; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KPFP 5
|| |
Db 1 KPSP 4

RESULT 36

TKNA_RANRI

ID TKNA_RANRI STANDARD; PRT; 11 AA.
 AC P29207;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranakinin (Substance-P-related peptide).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92044543; PubMed=1658233;
 RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
 RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
 RT neurokinin B from the brain of the frog Rana ridibunda."
 RL J. Neurochem. 57:2086-2091(1991).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 20.7%; Score 17; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KPFPK 6
 |||:
 Db 1 KPNPE 5

RESULT 37

TKND_RANCA

ID TKND_RANCA STANDARD; PRT; 11 AA.
 AC P22691;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatachykinin D (RTK D).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (*Rana catesbeiana*)
 RT brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=94023216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (*Rana catesbeiana*) brain and
 RT intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; D61033; D61033.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; FALSE_NEG.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 20.7%; Score 17; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPFPK 6
 |||:
 Db 1 KPNPE 5

RESULT 38

MP1_MICOC
 ID MP1_MICOC STANDARD; PRT; 13 AA.
 AC P81532;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE MP1 protein (Fragments).
 OS Microplitis ocellatae (Braconid wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidea;
 OC Braconidae; Microgastrinae; Microplitis.
 OX NCBI_TaxID=99573;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RA Takahashi M., Quicke D.L.J.;
 RL Submitted (OCT-1998) to Swiss-Prot.

CC -!- TISSUE SPECIFICITY: Salivary glands.

CC -!- DEVELOPMENTAL STAGE: LARVAL.

FT NON_CONS 10 11

SQ SEQUENCE 13 AA; 1595 MW; 0C0786C9DD82777B CRC64;

Query Match 20.7%; Score 17; DB 1; Length 13;

Best Local Similarity 66.7%; Pred. No. 6.5e+03;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5

|:|

Db 5 PYP 7

RESULT 39

NP2_LYMST

ID NP2_LYMST STANDARD; PRT; 13 AA.

AC P80179;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-JUL-1993 (Rel. 26, Last annotation update)

DE Lymna-DF-amide 2.

OS Lymnaea stagnalis (Great pond snail).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;

OC Lymnaeoidae; Lymnaeidae; Lymnaea.

OX NCBI_TaxID=6523;

RN [1]

RP SEQUENCE.

RC TISSUE=Ganglion;

RX MEDLINE=93238777; PubMed=8477756;

RA Johnsen A.H., Rehfeld J.F.;

RT "LymnaDFamides, a new family of neuropeptides from the pond snail,

RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in

RT invertebrates?";

RL Eur. J. Biochem. 213:875-879(1993).

CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.

DR PIR; S32472; S32472.

KW Neuropeptide; Amidation.

FT MOD_RES 13 13 AMIDATION.

FT UNSURE 8 8

SQ SEQUENCE 13 AA; 1492 MW; 9CA07BA3F5D5A5A5 CRC64;

Query Match 20.7%; Score 17; DB 1; Length 13;

Best Local Similarity 20.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PFPKLKVEVF 12

|: :: |

Db 1 PYDRISSSAF 10

RESULT 40

YPE2_LACLC

ID YPE2_LACLC STANDARD; PRT; 13 AA.

AC P42021;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein in PEPT 5'region (ORF2) (Fragment).
 OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94245610; PubMed=8188586;
 RA Mierau I., Haandrikman A.J., Velterop O., Tan P.S.T., Leenhouts K.L.,
 RA Konings W.N., Venema G., Kok J.;
 RT "Tripeptidase gene (pepT) of Lactococcus lactis: molecular cloning
 RT and nucleotide sequencing of pepT and construction of a chromosomal
 RT deletion mutant.";
 RL J. Bacteriol. 176:2854-2861(1994).

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; L27596; AAA20625.1; -.
 KW Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 13 AA; 1392 MW; 3671D53271B459D7 CRC64;

Query Match 20.7%; Score 17; DB 1; Length 13;
 Best Local Similarity 42.9%; Pred. No. 6.5e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKPFPKL 7
 :||| |
 Db 4 IEPFISL 10

RESULT 41

IF2G_RAT
 ID IF2G_RAT STANDARD; PRT; 14 AA.
 AC P81795;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Eukaryotic translation initiation factor 2 subunit 3 (Eukaryotic
 DE translation initiation factor 2 gamma subunit) (eIF-2-gamma) (PP42)
 DE (Fragment).
 GN EIF2S3 OR EIF2G.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=96374441; PubMed=8780732;
 RA Gil C., Plana M., Riera M., Itarte E.;

RT "Rat liver pp49, a protein that forms complexes with protein kinase
RT CK2, is composed of the beta and the gamma subunits of translation
RT initiation factor eIF-2.";
RL Biochem. Biophys. Res. Commun. 225:1052-1057(1996).
CC -!- FUNCTION: eIF-2 functions in the early steps of protein synthesis
CC by forming a ternary complex with GTP and initiator tRNA. This
CC complex binds to a 40s ribosomal subunit, followed by mRNA binding
CC to form a 43S preinitiation complex. Junction of the 60S ribosomal
CC subunit to form the 80S initiation complex is preceded by
CC hydrolysis of the GTP bound to eIF-2 and release of an eIF-2-GDP
CC binary complex. In order for eIF-2 to recycle and catalyze another
CC round of initiation, the GDP bound to eIF-2 must exchange with GTP
CC by way of a reaction catalyzed by eIF-2b.
CC -!- SUBUNIT: Heterotrimer composed of an alpha, a beta and a gamma
CC chain.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EIF2G subfamily.
KW Initiation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1511 MW; D86EDA955ABEFA12 CRC64;

Query Match 20.7%; Score 17; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KVEVFP 13
::||| |
Db 4 EIEVRP 9

RESULT 42
UC34_MAIZE
ID UC34_MAIZE STANDARD; PRT; 14 AA.
AC P80640;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 360)
DE (Fragments).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.7, its MW is: 41.1 kDa.
CC -!- CAUTION: The order of the peptides shown is uncertain.
DR Maize-2DPAGE; P80640; COLEOPTILE.

DR MaizeDB; 123965; -.
 FT NON_TER 1 1
 FT NON_CONS 8 9
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1527 MW; DC525FF7B0BE682D CRC64;

Query Match 20.7%; Score 17; DB 1; Length 14;
 Best Local Similarity 44.4%; Pred. No. 7e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 7 LKVEVFPFP 15
 | : || |
 Db 6 LALSVFDEP 14

RESULT 43

GTS_ASADI

ID GTS_ASADI STANDARD; PRT; 15 AA.
 AC P83246;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glutathione S-transferase (EC 2.5.1.18) (GST class-sigma) (adGST)
 DE (Fragment).
 OS Asaphis dichotoma.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
 OC Tellinoidea; Psammobiidae; Asaphis.
 OX NCBI_TaxID=184428;
 RN [1]
 RP SEQUENCE, FUNCTION, SUBUNIT, MASS SPECTROMETRY, AND CIRCULAR DICHROISM
 RP ANALYSIS.
 RC TISSUE=Intestine, and Liver;
 RX MEDLINE=22135252; PubMed=12139969;
 RA Yang H.-L., Nie L.-J., Zhu S.-G., Zhou X.-W.;
 RT "Purification and characterization of a novel glutathione S-
 RT transferase from Asaphis dichotoma."
 RL Arch. Biochem. Biophys. 403:202-208(2002).
 CC -!- FUNCTION: Has a strong specific activity toward 1-chloro-2,4-
 CC dinitrobenzene and etharynic acid.
 CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
 CC -!- SUBUNIT: Homodimer.
 CC -!- MASS SPECTROMETRY: MW=23138; METHOD=MALDI.
 CC -!- MISCELLANEOUS: In A.dichotoma there are at least two isozymes of
 CC glutathione S-transferase.
 CC -!- MISCELLANEOUS: Optimal pH is 8.5 with 1-chloro-2,4-dinitrobenzene
 CC as the substrate.
 CC -!- MISCELLANEOUS: The Km for 1-chloro-2,4-dinitrobenzene and
 CC glutathione are 0.68 +/-0.05 and 0.106 +/-0.005 mM, and the Vmax
 CC is 0.1446 +/-0.0072 and 0.033 +/-0.002 mmol/min x mg enzyme,
 CC respectively.
 CC -!- SIMILARITY: Belongs to the GST superfamily. Sigma family.
 DR GO; GO:0004364; F:glutathione transferase activity; NAS.
 DR GO; GO:0006803; P:glutathione conjugation reaction; NAS.
 KW Transferase.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1767 MW; CB3E4BF92D3CB0B9 CRC64;

Query Match 20.7%; Score 17; DB 1; Length 15;
Best Local Similarity 37.5%; Pred. No. 7.5e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PKLKVEVF 12
| |:
Db 1 PSYKLHYF 8

RESULT 44

UC17_MAIZE

ID UC17_MAIZE STANDARD; PRT; 15 AA.
AC P80623;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 32)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.5, its MW is: 42.7 kDa.
DR Maize-2DPAGE; P80623; COLEOPTILE.
DR MaizeDB; 123949; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1554 MW; C0AFFF15FFECEEC8 CRC64;

Query Match 20.7%; Score 17; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 7.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 LKVEVF 12
| | ||
Db 2 LSPVPF 7

RESULT 45

UC29_MAIZE

ID UC29_MAIZE STANDARD; PRT; 15 AA.
AC P80635;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)
DE (Fragment).

OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.9, its MW is: 37.6 kDa.
 DR Maize-2DPAGE; P80635; COLEOPTILE.
 DR MaizeDB; 123960; -.
 FT NON TER 1 1
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;

 Query Match 20.7%; Score 17; DB 1; Length 15;
 Best Local Similarity 25.0%; Pred. No. 7.5e+03;
 Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

 QY 3 PFPKLVKE 10
 | | : ::
 Db 6 PIPLVDID 13

RESULT 46

H2B3_ICTPU

ID H2B3_ICTPU STANDARD; PRT; 17 AA.
 AC P81904;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Histone H2B-3 (Antibacterial histone-like protein 3) (HLP-3)
 DE (Fragment).
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OX NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Skin;
 RX MEDLINE=98309109; PubMed=9645227;
 RA Robinette D., Wada S., Arroll T., Levy M.G., Miller W.L., Noga E.J.;
 RT "Antimicrobial activity in the skin of the channel catfish Ictalurus
 RT punctatus: characterization of broad-spectrum histone-like
 RT antimicrobial proteins.";
 RL Cell. Mol. Life Sci. 54:467-475(1998).
 CC -!- FUNCTION: Has antimicrobial activity. Possesses strong activity
 CC against saprolegnia, the most common fungal infection in fish.
 CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules
 CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146

CC bp of DNA.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- MASS SPECTROMETRY: MW=13506; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the histone H2B family.
 DR InterPro; IPR000558; Histone_H2B.
 DR PROSITE; PS00357; HISTONE_H2B; PARTIAL.
 KW Nuclear protein; Chromosomal protein; Nucleosome core; DNA-binding;
 KW Antibiotic; Fungicide.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1795 MW; 44FB8D966FD2F377 CRC64;

Query Match 20.7%; Score 17; DB 1; Length 17;
 Best Local Similarity 57.1%; Pred. No. 8.4e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KPFPKLLK 8
 | |||
 Db 5 KTAPKKK 11

RESULT 47

LMT3_LOCFMI

ID LMT3_LOCFMI STANDARD; PRT; 9 AA.
 AC P41489;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustamyotropin 3 (LOM-MT-3).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
 RA de Loof A.;
 RT "Isolation, identification and synthesis of locustamyotropin III and
 RT IV, two additional neuropeptides of Locusta migratoria: members of the
 RT locustamyotropin peptide family."
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).
 CC -!- FUNCTION: Potent mediator of visceral muscle contractile activity
 CC (myotropic activity).
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR PIR; A61620; A61620.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 20.1%; Score 16.5; DB 1; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.4e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

Qy 2 KPF-PKL 7

Db : || | : |
3 QPFVPERL 9

RESULT 48

UBL1_MONDO

ID UBL1_MONDO STANDARD; PRT; 15 AA.
AC P50103;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-
DE L1) (Ubiquitin thiolesterase L1) (Neuron cytoplasmic protein 9.5)
DE (PGP 9.5) (PGP9.5) (Fragment).
GN UCHL1.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxID=13616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96102916; PubMed=8522974;
RA Mann D.A., Trowern A.R., Lavender F.L., Whittaker P.A.,
RA Thompson R.J.;
RT "Identification of evolutionary conserved regulatory sequences in the
RT 5' untranscribed region of the neural-specific ubiquitin C-terminal
RT hydrolase (PGP9:5) gene.";
RL J. Neurochem. 66:35-46(1996).
CC -!- FUNCTION: Ubiquitin-protein hydrolase is involved both in the
CC processing of ubiquitin precursors and of ubiquitinated proteins.
CC This enzyme is a thiol protease that recognizes and hydrolyzes
CC a peptide bond at the C-terminal glycine of ubiquitin.
CC -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + a thiol.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to peptidase family C12.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U32208; AAA89059.1; -.
DR InterPro; IPR001578; Peptidase_C12.
DR PROSITE; PS00140; UCH_1; PARTIAL.
KW Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1816 MW; 1B7A3B6E623F6E79.CRC64;

Query Match 20.1%; Score 16.5; DB 1; Length 15;
Best Local Similarity 38.5%; Pred. No. 9e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 5; Gaps 1;

Qy 1 LKPFPKLKVEVFP 13
 ||| :|: |
 Db 3 LKP-----MEINP 10

RESULT 49

LPK1_LOCMI

ID LPK1_LOCMI STANDARD; PRT; 16 AA.
 AC P20404;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Locustapyrokinin 1 (LOM-PK-1).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=91224474; PubMed=2026322;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
 RT myotropic peptide of Locusta migratoria."
 RL Gen. Comp. Endocrinol. 81:97-104(1991).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR PIR; A49761; A49761.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 16 16 AMIDATION.
 SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;

Query Match 20.1%; Score 16.5; DB 1; Length 16;
 Best Local Similarity 57.1%; Pred. No. 9.5e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

Qy 2 KPF-PKL 7
 :|| |:|
 Db 10 QPFVPRL 16

RESULT 50

BPP2_BOTIN

ID BPP2_BOTIN STANDARD; PRT; 10 AA.
 AC P30422;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom."
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; B37196; B37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 19.5%; Score 16; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 7.3e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PFPKL 7
 | |::
 Db 4 PHPQI 8

Search completed: July 4, 2004, 04:41:31
 Job time : 5.14925 secs